

TABLE 3B					
Genes Corresponding to Differentially Expressed Genes in Figure 9 - Obesity					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1	0.041454	vacuolar protein sorting 28 (yeast) (VPS28), mRNA /cds=(62,727) /gb=NM_016208 /gi=7705884 /ug=Hs.339697 /len=928	NM_016208	Hs.339697	NP_057292
214	0.02042	neuronal thread protein AD7c-NTP	NP_055301		
257	0.005038	KIAA0301 gene, partial cds	AB002299		NP_055426
288	0.002317	phosphodiesterase 8B (PDE8B), mRNA /cds=(46,2703) /gb=NM_003719 /gi=26006850 /ug=Hs.78106 /len=3567	NM_003719	Hs.78106	NP_003710
298	0.025168	KIAA0429 gene product (KIAA0429), mRNA /cds=(2374,3444) /gb=NM_014751 /gi=7662113 /ug=Hs.77694 /len=5645	NM_014751	Hs.77694	NP_055566
323	0.005852	associated molecule with the SH3 domain of STAM (AMSH), mRNA /cds=(188,1462) /gb=NM_006463 /gi=17738303 /ug=Hs.12479 /len=2107	NM_006463	Hs.12479	NP_006454
357	0.007162	deleted in pancreatic carcinoma (DPC4) gene, exon 3	AF045440		
383	0.031506	zinc finger protein 223 (ZNF223), mRNA /cds=(239,1687) /gb=NM_013361 /gi=7019588 /ug=Hs.279782 /len=2033	NM_013361	Hs.279782	NP_037493
423	0.012975	biotinidase (BTD), mRNA /cds=(36,1667) /gb=NM_000060 /gi=4557372 /ug=Hs.78885 /len=2016	NM_000060	Hs.78885	NP_000051
429	0.026411	NPD009 protein (NPD009), mRNA /cds=(1327,1677) /gb=NM_020686 /gi=24476005 /ug=Hs.283675 /len=2514	NM_020686	Hs.283675	NP_065737
434	0.012537	phosphoglycerate kinase 1 (PGK1), mRNA /cds=(70,1323) /gb=NM_000291 /gi=22095338 /ug=Hs.78771 /len=2338	NM_000291	Hs.78771	NP_000282
450	0.028189	nuclear factor NF-IL6	X52560		
453	0.012175	WD repeat domain 1 (WDR1), transcript variant 1, mRNA /cds=(203,2023) /gb=NM_017491 /gi=17105397 /ug=Hs.85100 /len=3079	NM_017491	Hs.85100	NP_059830
477	0.034563	microfibrillar-associated protein 4 (MFAP4), mRNA /cds=(26,793) /gb=NM_002404 /gi=23111004 /ug=Hs.296049 /len=1830	NM_002404	Hs.296049	NP_002395
512	0.001459	myosin IXB (MYO9B), mRNA /cds=(1,6069) /gb=NM_004145 /gi=4758749 /ug=Hs.159629 /len=6069	NM_004145	Hs.159629	NP_004136
565	0.022932	topoisomerase (DNA) III alpha (TOP3A), mRNA /cds=(230,3235) /gb=NM_004618 /gi=20143947 /ug=Hs.91175 /len=3807	NM_004618	Hs.91175	NP_004609

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
579	0.046542	Rad50-interacting protein 1 (FLJ11785), mRNA /cds=(24,2489) /gb=NM_021930 /gi=19923579 /ug=Hs.44625 /len=2855	NM_021930	Hs.44625	NP_068749
584	0.036865	isocitrate dehydrogenase 1 (NADP), soluble (IDH1), mRNA /cds=(235,1479) /gb=NM_005896 /gi=28178824 /ug=Hs.11223 /len=2339	NM_005896	Hs.11223	NP_005887
589	0.037157	AGENCOURT_6640990 NIH_MGC_68 cDNA clone IMAGE:5735856 5', mRNA sequence /clone=IMAGE:5735856 /clone_end=5' /gb=BM907553 /gi=19357932 /ug=Hs.424427 /len=645	BM907553	Hs.424427	
613	0.047341	PEF protein with a long N-terminal hydrophobic domain (peflin) (PEF), mRNA /cds=(13,867) /gb=NM_012392 /gi=6912581 /ug=Hs.241531 /len=1641	NM_012392	Hs.241531	NP_036524
615	0.041872	cDNA FLJ11904 fis, clone HEMBB1000048. /gb=AK021966 /gi=10433275 /ug=Hs.285519 /len=2134	AK021966	Hs.285519	
617	0.049654	solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10), mRNA /cds=(251,1876) /gb=NM_030777 /gi=21361923 /ug=Hs.305971 /len=4396	NM_030777	Hs.305971	NP_110404
625	0.005892	fragile X mental retardation 1 (FMR1), mRNA /cds=(220,2118) /gb=NM_002024 /gi=4503764 /ug=Hs.89764 /len=4362	NM_002024	Hs.89764	NP_002015
627	0.017523	methionine-tRNA synthetase (MARS), mRNA /cds=(24,2726) /gb=NM_004990 /gi=14043021 /ug=Hs.279946 /len=2795	NM_004990	Hs.279946	NP_004981
634	0.020686	mitofusin 1 (MFN1), transcript variant 1, mRNA /cds=(84,2309) /gb=NM_033540 /gi=16117784 /ug=Hs.197877 /len=3275	NM_033540	Hs.197877	NP_284941
652	0.01004	cDNA FLJ38331 fis, clone FCBBF3025285, moderately similar to Mus musculus peripheral benzodiazepine receptor associated protein (Pap7) mRNA. /gb=AK095650 /gi=21754954 /ug=Hs.9052 /len=3547	AK095650	Hs.9052	
657	0.00593	FLJ30577 fis, clone BRAWH2006760 /cds=UNKNOWN /gb=AK055139 /gi=16549803 /ug=Hs.324815 /len=2353	AK055139	Hs.324815	
658	0.029283	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705	NM_006855	Hs.250696	NP_057839

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
662	0.005051	insulin-like growth factor binding protein 5 (IGFBP5), mRNA /cds=(752,1570) /gb=NM_000599 /gi=10834981 /ug=Hs.380833 /len=1722	NM_000599	Hs.380833	NP_000590
668	0.035062	KIAA0391 gene product (KIAA0391), mRNA /cds=(360,2063) /gb=NM_014672 /gi=7662093 /ug=Hs.154668 /len=5677	NM_014672	Hs.154668	NP_055487
670	0.036456	cytidine deaminase (CDA), mRNA /cds=(118,558) /gb=NM_001785 /gi=11386156 /ug=Hs.72924 /len=892	NM_001785	Hs.72924	NP_001776
691	0.014281	U5 snRNP-specific protein, 200-KD (U5-200KD), mRNA /cds=(189,5624) /gb=NM_014014 /gi=24307974 /ug=Hs.246112 /len=5898	NM_014014	Hs.246112	NP_054733
693	9.54E-04	ubiquitin-conjugating enzyme E2L 3 (UBE2L3), mRNA /cds=(16,480) /gb=NM_003347 /gi=4507788 /ug=Hs.108104 /len=2845	NM_003347	Hs.108104	NP_003338
697	0.044049	interferon, alpha-inducible protein (clone IFI-6-16) (G1P3), transcript variant 3, mRNA /cds=(108,524) /gb=NM_022873 /gi=13259549 /ug=Hs.265827 /len=841	NM_022873	Hs.265827	NP_075011
721	9.54E-04	mitochondrion, complete genome	NC_001807		
726	1.64E-04	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747	NM_012479	Hs.25001	NP_036611
772	0.001525	acid sphingomyelinase (ASM) gene, exons a, and alternative a (3' end), b and c (5' end).	M59917		
787	0.008356	cargo selection protein (mannose 6 phosphate receptor binding protein) (TIP47), mRNA /cds=(67,1371) /gb=NM_005817 /gi=20127485 /ug=Hs.140452 /len=2239	NM_005817	Hs.140452	NP_005808
793	0.012175	glyoxalase I (GLO1), mRNA /cds=(88,642) /gb=NM_006708 /gi=5729841 /ug=Hs.75207 /len=1993	NM_006708	Hs.75207	NP_006699
794	0.004048	zn87g06.x5 Stratagene lung carcinoma 937218 cDNA clone IMAGE:565210 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;, mRNA sequence /clone=IMAGE:565210 /clone_end=3' /gb=AI732466 /gi=5053579 /ug=Hs.193133 /len=526	AI732466	Hs.193133	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
807	0.017281	KIAA0102 gene product (KIAA0102), mRNA /cds=(308,679) /gb=NM_014752 /gi=7661907 /ug=Hs.77665 /len=1370	NM_014752	Hs.77665	NP_055567
808	0.005051	PIX1 mRNA (ORF)	AF037219		NP_570854
809	0.003193	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) (MCCC1), mRNA /cds=(133,2310) /gb=NM_020166 /gi=13518227 /ug=Hs.47649 /len=2528	NM_020166	Hs.47649	NP_064551
831	0.039115	Microfibril-associated glycoprotein-2 (MAGP2), mRNA /cds=(214,735) /gb=NM_003480 /gi=4505088 /ug=Hs.300946 /len=1119	NM_003480	Hs.300946	NP_003471
837	0.007261	serine/arginine repetitive matrix 2 (SRRM2), mRNA /cds=(226,8484) /gb=NM_016333 /gi=19923465 /ug=Hs.197114 /len=9027	NM_016333	Hs.197114	NP_057417
847	0.037157	peroxisomal biogenesis factor 3 (PEX3), mRNA /cds=(64,1185) /gb=NM_003630 /gi=4505726 /ug=Hs.7277 /len=1979	NM_003630	Hs.7277	NP_003621
851	6.22E-04	of89c05.s1 NCI_CGAP_Li5 cDNA clone IMAGE:1437512 3' similar to contains Alu repetitive element; mRNA sequence /clone=IMAGE:1437512 /clone_end=3' /gb=AA894384 /gi=3030785 /ug=Hs.432123 /len=296	AA894384	Hs.432123	
865	0.001133	mitochondrion, complete genome	NC_001807		
877	0.006234	ring finger protein 11 (RNF11), mRNA /cds=(128,592) /gb=NM_014372 /gi=7657519 /ug=Hs.96334 /len=2529	NM_014372	Hs.96334	NP_055187
909	0.026411	integral membrane protein Tmp21-I (p23)	AJ004913		NP_006818
918	0.001283	AGENCOURT_6456859 NIH_MGC_92 cDNA clone IMAGE:5576908 5', mRNA sequence /clone=IMAGE:5576908 /clone_end=5' /gb=BM466169 /gi=18515211 /ug=Hs.439148 /len=1150	BM466169	Hs.439148	
921	0.012975	mitochondrion, complete genome	NC_001807		
923	0.013819	eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa (EIF3S3), mRNA /cds=(6,1064) /gb=NM_003756 /gi=4503514 /ug=Hs.58189 /len=1280	NM_003756	Hs.58189	NP_003747
930	0.008208	FK506 binding protein 9, 63 kDa (FKBP9), mRNA /cds=(457,885) /gb=NM_007270 /gi=24307926 /ug=Hs.302749 /len=2517	NM_007270	Hs.302749	NP_009201
931	0.041454	signal recognition particle 54kDa (SRP54), mRNA /cds=(225,1739) /gb=NM_003136 /gi=20149548 /ug=Hs.49346 /len=2164	NM_003136	Hs.49346	NP_003127

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943	0.004687	XIST, coding sequence "a" mRNA (locus DXS399E). /gb=X56199 /gi=37987 /ug=Hs.352403 /len=1614	X56199	Hs.352403	
954	0.029809	cell cycle progression 8 protein (CPR8), mRNA /cds=(13,1140) /gb=NM_004748 /gi=4758047 /ug=Hs.82506 /len=1856	NM_004748	Hs.82506	NP_004739
980	0.033283	cleavage and polyadenylation specific factor 6, 68kDa (CPSF6), mRNA /cds=(35,1690) /gb=NM_007007 /gi=5901927 /ug=Hs.64542 /len=3426	NM_007007	Hs.64542	NP_008938
998	0.017682	down-regulator of transcription 1, TBP-binding (negative cofactor 2) (DR1), mRNA /cds=(548,1078) /gb=NM_001938 /gi=4503380 /ug=Hs.16697 /len=1375	NM_001938	Hs.16697	NP_001929
1001	0.031506	RAD23 B (S. cerevisiae) (RAD23B), mRNA /cds=(352,1581) /gb=NM_002874 /gi=19924138 /ug=Hs.404283 /len=2943	NM_002874	Hs.404283	NP_002865
1008	0.039257	Alg5, S. cerevisiae, of (ALG5), mRNA /cds=(28,1002) /gb=NM_013338 /gi=9665250 /ug=Hs.227933 /len=1125	NM_013338	Hs.227933	NP_037470
1015	0.013819	actinin, alpha 1 (ACTN1), mRNA /cds=(184,2862) /gb=NM_001102 /gi=12025669 /ug=Hs.119000 /len=3398	NM_001102	Hs.119000	NP_001093
1021	0.015649	tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA /cds=(67,2439) /gb=NM_006290 /gi=26051241 /ug=Hs.211600 /len=4446	NM_006290	Hs.211600	NP_006281
1023	0.022422	v-fos FBJ murine osteosarcoma viral oncogene (FOS), mRNA /cds=(156,1298) /gb=NM_005252 /gi=6552332 /ug=Hs.25647 /len=2084	NM_005252	Hs.25647	NP_005243
1026	0.023762	methionine adenosyltransferase II, beta (MAT2B), mRNA /cds=(73,1077) /gb=NM_013283 /gi=20127525 /ug=Hs.54642 /len=2054	NM_013283	Hs.54642	NP_037415
1028	0.025168	ATP synthase, H transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417	NM_006886	Hs.177530	NP_008817
1036	0.031506	mRNA for KIAA1518 protein, partial cds. /cds=(482,3112) /gb=AB040951 /gi=7959302 /ug=Hs.284208 /len=5370	AB040951	Hs.284208	NP_056308
1051	0.029809	HSPC133 protein (HSPC133), mRNA /cds=(83,481) /gb=NM_014168 /gi=7661791 /ug=Hs.273063 /len=963	NM_014168	Hs.273063	NP_054887

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1080	0.026411	Similar to RIKEN cDNA 4833424O15 gene, clone IMAGE:4793707, mRNA /gb=BC040174 /gi=25777829 /ug=Hs.312481 /len=3745	BC040174	Hs.312481	
1120	0.046149	clone 25032 mRNA sequence /cds=UNKNOWN /gb=AF131764 /gi=4406586 /ug=Hs.13399 /len=1798	AF131764	Hs.13399	NP_071919
1168	0.002566	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556	NM_021109	Hs.75968	NP_066932
1170	0.017682	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_079425	Hs.77385	NP_524149
1174	0.025168	eukaryotic translation initiation factor 3, subunit 6 interacting protein (EIF3S6IP), mRNA /cds=(34,1728) /gb=NM_016091 /gi=7705432 /ug=Hs.119503 /len=1901	NM_016091	Hs.119503	NP_057175
1189	0.00181	mRNA; cDNA DKFZp451A142 (from clone DKFZp451A142) /cds=(39,1898) /gb=AL834245 /gi=21739785 /ug=Hs.124918 /len=4902	AL834245	Hs.124918	
1193	0.031405	CGI-100 protein (CGI-100), mRNA /cds=(113,802) /gb=NM_016040 /gi=19923441 /ug=Hs.348996 /len=3635	NM_016040	Hs.348996	NP_057124
1194	0.013385	proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA /cds=(86,811) /gb=NM_002790 /gi=23110941 /ug=Hs.76913 /len=1023	NM_002790	Hs.76913	NP_002781
1236	0.037084	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) (MMP9), mRNA /cds=(20,2143) /gb=NM_004994 /gi=4826835 /ug=Hs.151738 /len=2334	NM_004994	Hs.151738	NP_004985
1267	0.008955	hypothetical protein DKFZp586K0717 (DKFZP586K0717), mRNA /cds=(168,1730) /gb=NM_030917 /gi=13569873 /ug=Hs.334812 /len=1914	NM_030917	Hs.334812	NP_112179
1301	0.003233	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
1305	0.037084	cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA /cds=(90,281) /gb=NM_001867 /gi=18105039 /ug=Hs.430075 /len=448	NM_001867	Hs.430075	NP_001858

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1306	0.023762	poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA /cds=(503,2404) /gb=NM_002568 /gi=4505574 /ug=Hs.172182 /len=2848	NM_002568	Hs.172182	NP_002559
1343	0.033283	hypothetical protein FLJ12438 (FLJ12438), mRNA /cds=(174,1340) /gb=NM_021933 /gi=11345471 /ug=Hs.8595 /len=1575	NM_021933	Hs.8595	NP_068752
1349	0.009309	mRNA; cDNA DKFZp313D2314 (from clone DKFZp313D2314) /gb=AL832057 /gi=21732598 /ug=Hs.3685 /len=3141	AL832057	Hs.3685	
1386	0.034454	AGENCOURT_6424254 NIH_MGC_67 cDNA clone IMAGE:5491531 5', mRNA sequence /clone=IMAGE:5491531 /clone_end=5' /gb=BM479954 /gi=18528996 /ug=Hs.381243 /len=1112	BM479954	Hs.381243	
1418	0.013819	voltage-dependent anion channel 2 (VDAC2), mRNA /cds=(63,947) /gb=NM_003375 /gi=4507880 /ug=Hs.78902 /len=1404	NM_003375	Hs.78902	NP_003366
1419	0.017682	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) (CD74), mRNA /cds=(8,706) /gb=NM_004355 /gi=10835070 /ug=Hs.84298 /len=1304	NM_004355	Hs.84298	NP_004346
1431	0.011417	inhibitor of growth family, member 1 (ING1), mRNA /cds=(433,1701) /gb=NM_005537 /gi=19923770 /ug=Hs.46700 /len=2886	NM_005537	Hs.46700	NP_005528
1450	0.039115	EST384321 MAGE resequences, MAGL cDNA, mRNA sequence /gb=AW972232 /gi=8162078 /ug=Hs.152375 /len=617	AW972232	Hs.152375	
1455	0.013385	CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA /cds=(260,2668) /gb=NM_001253 /gi=16357499 /ug=Hs.155174 /len=3012	NM_001253	Hs.155174	NP_001244
1467	0.037084	SON DNA binding protein (SON), transcript variant e, mRNA /cds=(50,6376) /gb=NM_058183 /gi=21040317 /ug=Hs.92909 /len=8482	NM_058183	Hs.92909	NP_620305
1469	0.016639	potassium channel modulatory factor (PCMF), mRNA /cds=(54,1199) /gb=NM_020122 /gi=10047127 /ug=Hs.5392 /len=1595	NM_020122	Hs.5392	NP_064507
1497	0.005439	hypothetical protein MGC45474 (MGC45474), mRNA /cds=(218,2035) /gb=NM_152369 /gi=22748794 /ug=Hs.234101 /len=2384	NM_152369	Hs.234101	
1500	0.031405	KIAA0824 (=PCF11p homolog)	AB020631		NP_056969

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1535	0.004048	mRNA for KIAA0752 protein, partial cds. /cds=(1,1006) /gb=AB018295 /gi=3882224 /ug=Hs.126779 /len=4332	AB018295	Hs.126779	NP_775934
1539	0.00295	LENG5 protein (LENG5), mRNA /cds=(113,1285) /gb=NM_024075 /gi=13129061 /ug=Hs.15580 /len=1364	NM_024075	Hs.15580	NP_076980
1574	0.019933	similar to triple functional domain (PTPRF interacting) (LOC115557), mRNA /cds=(331,1755) /gb=NM_133483 /gi=19311007 /ug=Hs.61581 /len=2166	NM_133483	Hs.61581	NP_597840
1577	0.045762	POM121 membrane glycoprotein (rat) (POM121), mRNA /cds=(978,3932) /gb=NM_172020 /gi=26051277 /ug=Hs.295112 /len=6014	NM_172020	Hs.295112	NP_742017
1651	0.035141	zinc finger protein 384 (ZNF384), mRNA /cds=(499,2229) /gb=NM_133476 /gi=20143968 /ug=Hs.103315 /len=3291	NM_133476	Hs.103315	NP_597733
1665	0.026411	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
1673	0.043451	endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 (HERPUD1), mRNA /cds=(96,1271) /gb=NM_014685 /gi=7661869 /ug=Hs.146393 /len=1884	NM_014685	Hs.146393	NP_055500
1709	0.048172	KIAA0399	AB007859		NP_055928
1724	8.74E-04	zinc finger RNA binding protein (ZFR), mRNA /cds=(44,1300) /gb=NM_016107 /gi=7706372 /ug=Hs.173518 /len=2734	NM_016107	Hs.173518	NP_057191
1751	0.039257	insulin induced protein 2 (LOC51141), mRNA /cds=(141,857) /gb=NM_016133 /gi=23821030 /ug=Hs.7089 /len=1358	NM_016133	Hs.7089	NP_057217
1756	0.013819	uronyl-2-sulfotransferase (UST), mRNA /cds=(104,1324) /gb=NM_005715 /gi=5032218 /ug=Hs.134015 /len=4196	NM_005715	Hs.134015	NP_005706
1830	0.033283	calmodulin-I (CALM1) mRNA, 3'UTR, partial sequence. /gb=U16850 /gi=576644 /ug=Hs.374441 /len=2383	U16850	Hs.374441	
1927	0.036435	EST (tg16b07.x1 NCI_CGAP_CLL1 clone IMAGE:2108917 3' TR:Q14526 Q14526 HIC-1 GENE FRAGMENT)	AI391567		NP_006488
1974	0.045762	CDC20 cell division cycle 20 (S. cerevisiae) (CDC20), mRNA /cds=(111,1610) /gb=NM_001255 /gi=4557436 /ug=Hs.82906 /len=1686	NM_001255	Hs.82906	NP_001246

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1988	0.029809	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) (ST13), mRNA /cds=(144,1253) /gb=NM_003932 /gi=21237722 /ug=Hs.119222 /len=3214	NM_003932	Hs.119222	NP_003923
2033	0.012175	calmodulin 1 (phosphorylase kinase, delta) (CALM1), mRNA /cds=(200,649) /gb=NM_006888 /gi=5901911 /ug=Hs.282410 /len=1526	NM_006888	Hs.282410	NP_008819
2036	0.041237	ATPase, H transporting, lysosomal 56/58kDa, V1 subunit B, isoform 2 (ATP6V1B2), mRNA /cds=(208,1743) /gb=NM_001693 /gi=19913427 /ug=Hs.1697 /len=3054	NM_001693	Hs.1697	NP_001684
2041	0.048653	ribosomal protein L32 (RPL32), mRNA /cds=(51,458) /gb=NM_000994 /gi=15812220 /ug=Hs.169793 /len=521	NM_000994	Hs.169793	NP_000985
2073	0.002372	transcription factor B1, mitochondrial (TFB1M), mRNA /cds=(73,1113) /gb=NM_016020 /gi=7705784 /ug=Hs.279908 /len=1290	NM_016020	Hs.279908	NP_057104
2074	0.039115	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) (CLU), mRNA /cds=(48,1397) /gb=NM_001831 /gi=4502904 /ug=Hs.75106 /len=1676	NM_001831	Hs.75106	NP_001822
2077	0.019933	musculus exoribonuclease 1 (Xrn1)	NM_011916		NP_036046
2105	0.041237	potassium channel, subfamily K, member 1 (KCNK1), mRNA /cds=(183,1193) /gb=NM_002245 /gi=15451900 /ug=Hs.79351 /len=1901	NM_002245	Hs.79351	NP_002236
2175	0.025168	clone IMAGE:4799018, mRNA /gb=BC045722 /gi=28277129 /ug=Hs.153527 /len=2587	BC045722	Hs.153527	
2194	0.011417	monocytic leukemia zinc finger protein-related factor (MORF), mRNA /cds=(316,6537) /gb=NM_012330 /gi=6912511 /ug=Hs.27590 /len=6537	NM_012330	Hs.27590	NP_036462
2211	0.017682	L-isoaspartyl/D-aspartyl O-methyltransferase (PCMT1) gene, exon 1,	U49740		
2230	0.041237	PMS1 postmeiotic segregation increased 1 (S. cerevisiae) (PMS1), mRNA /cds=(81,2879) /gb=NM_000534 /gi=11496979 /ug=Hs.111749 /len=3121	NM_000534	Hs.111749	NP_000525
2231	0.026643	TTN gene for titin	AJ277892		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2242	0.031506	uncharacterized hypothalamus protein HT010 (HT010), mRNA /cds=(227,1420) /gb=NM_018471 /gi=8923807 /ug=Hs.6375 /len=2140	NM_018471	Hs.6375	NP_060941
2273	0.033283	Pirin (PIR), mRNA /cds=(231,1103) /gb=NM_003662 /gi=4505822 /ug=Hs.424966 /len=1318	NM_003662	Hs.424966	NP_003653
2303	0.035141	cDNA FLJ13446 fis, clone PLACE1002968. /gb=AK023508 /gi=10435460 /ug=Hs.201925 /len=1712	AK023508	Hs.201925	
2307	0.002773	matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=NM_002381 /gi=13518040 /ug=Hs.278461 /len=2599	NM_002381	Hs.278461	NP_002372
2309	0.025168	GTPase-activating protein GAP111	U20238		NP_033051
2317	0.006234	mRNA for KIAA0570 protein, partial cds. /cds=(480,10718) /gb=AB011142 /gi=20521084 /ug=Hs.180948 /len=11269	AB011142	Hs.180948	
2318	0.045762	mRNA for KIAA0611 protein, partial cds. /cds=(1,2740) /gb=AB014511 /gi=3327035 /ug=Hs.406434 /len=7176	AB014511	Hs.406434	
2480	0.025168	topoisomerase (DNA) I (TOP1), mRNA /cds=(247,2544) /gb=NM_003286 /gi=19913404 /ug=Hs.317 /len=3734	NM_003286	Hs.317	NP_003277
2506	0.022422	bHLH-PAS transcription factor MOP9 (MOP9) mRNA, long form, complete cds, alternatively spliced /cds=(58,1815) /gb=AF231338 /gi=7963663 /ug=Hs.222024 /len=2008	AF231338	Hs.222024	NP_064568
2542	0.039115	leucyl-tRNA synthetase (LARS), mRNA /cds=(73,3603) /gb=NM_020117 /gi=24496788 /ug=Hs.6762 /len=4248	NM_020117	Hs.6762	NP_064502
2557	0.03939	leucine-rich PPR-motif containing (LRPPRC), mRNA /cds=(46,3867) /gb=NM_133259 /gi=18959201 /ug=Hs.182490 /len=4782	NM_133259	Hs.182490	NP_573566
2625	0.033283	hypothetical protein (KIAA0714)	AB018257		
2652	0.013819	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 2b, mRNA /cds=(229,2481) /gb=NM_007289 /gi=6042203 /ug=Hs.1298 /len=5725	NM_007289	Hs.1298	NP_009220
2678	0.010023	protein-L-isoaspartate (D-aspartate) O-methyltransferase (PCMT1), mRNA /cds=(74,757) /gb=NM_005389 /gi=4885538 /ug=Hs.79137 /len=1599	NM_005389	Hs.79137	NP_005380

Spot	p-value	Déscription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2687	0.019933	v-fos FBJ murine osteosarcoma viral oncogene (FOS), mRNA /cds=(156,1298) /gb=NM_005252 /gi=6552332 /ug=Hs.25647 /len=2084	NM_005252	Hs.25647	NP_005243
2713	0.033283	caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 CAV1	AJ133269		
2741	0.010023	golgi SNAP receptor complex member 1 (GOSR1), mRNA /cds=(13,765) /gb=NM_004871 /gi=4758455 /ug=Hs.8868 /len=999	NM_004871	Hs.8868	NP_004862
2743	0.039115	clone MGC:9947 IMAGE:3876105, mRNA, complete cds /cds=(51,2216) /gb=BC013590 /gi=15488925 /ug=Hs.2437 /len=2651	BC013590	Hs.2437	
2745	0.035141	calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	AF223391		
2779	0.009383	nuclear factor (erythroid-derived 2)-like 2 (NFE2L2), mRNA /cds=(114,1931) /gb=NM_006164 /gi=20149575 /ug=Hs.155396 /len=2439	NM_006164	Hs.155396	NP_006155
2782	0.005811	high mobility group 2 protein (HMG-2)	M83665		
2797	0.028189	zinc finger homeobox 1b (ZFHX1B), mRNA /cds=(445,4089) /gb=NM_014795 /gi=7662183 /ug=Hs.34871 /len=5523	NM_014795	Hs.34871	NP_055610
2815	0.006684	proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6), mRNA /cds=(110,850) /gb=NM_002791 /gi=23110943 /ug=Hs.410276 /len=1035	NM_002791	Hs.410276	NP_002782
2843	0.002372	UI-E-EJ0-ahj-n-19-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahj-n-19-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahj-n-19-0-UI /clone_end=5' /gb=BM701108 /gi=19014366 /ug=Hs.401941 /len=1923	BM701108	Hs.401941	
2848	0.006234	BJ-HCC-24 tumor antigen mRNA, complete cds /cds=(2,1240) /gb=AY121805 /gi=22002585 /ug=Hs.433489 /len=1488	AY121805	Hs.433489	
2849	0.008208	chromosome 14 open reading frame 2 (C14orf2), mRNA /cds=(61,237) /gb=NM_004894 /gi=4758939 /ug=Hs.109052 /len=627	NM_004894	Hs.109052	NP_004885
2850	0.009383	helicase II (RAD54L) mRNA, complete cds. /cds=(54,4979) /gb=U09820 /gi=606832 /ug=Hs.96264 /len=6115	U09820	Hs.96264	NP_612115
2870	0.029809	threonyl-tRNA synthetase (TARS), mRNA /cds=(135,2270) /gb=NM_152295 /gi=25054078 /ug=Hs.84131 /len=2662	NM_152295	Hs.84131	NP_689508

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2875	0.043451	deubiquitinating enzyme (UNPH4)= AF153604 ubiquitin-specific protease homolog (UPH)	AF106069		NP_006304
2884	0.035141	mitochondrial ribosomal protein S30 (MRPS30), mRNA /cds=(39,1358) /gb=NM_016640 /gi=16950598 /ug=Hs.28555 /len=1482	NM_016640	Hs.28555	NP_057724
2910	0.026643	Sm protein F (LSM6), mRNA /cds=(82,324) /gb=NM_007080 /gi=5901997 /ug=Hs.42438 /len=596	NM_007080	Hs.42438	NP_009011
2913	9.20E-05	mortality factor 4 like 1 (MORF4L1), mRNA /cds=(132,1103) /gb=NM_006791 /gi=5803101 /ug=Hs.6353 /len=1766	NM_006791	Hs.6353	NP_006782
2928	0.022422	ligase IV, DNA, ATP-dependent (LIG4), mRNA /cds=(274,3009) /gb=NM_002312 /gi=23199992 /ug=Hs.166091 /len=3325	NM_002312	Hs.166091	NP_002303
2947	0.011417	hemoglobin, alpha 2 (HBA2), mRNA /cds=(38,466) /gb=NM_000517 /gi=14043068 /ug=Hs.347939 /len=575	NM_000517	Hs.347939	NP_000508
2967	0.016639	matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) (MMP2), mRNA /cds=(290,2272) /gb=NM_004530 /gi=11342665 /ug=Hs.111301 /len=3069	NM_004530	Hs.111301	NP_004521
2990	0.033283	cDNA FLJ31057 fis, clone HSYRA2000787. /gb=AK055619 /gi=16550395 /ug=Hs.296261 /len=2168	AK055619	Hs.296261	
3011	0.035141	mitochondrion, complete genome	NC_001807		
3029	0.022422	Yip1p-interacting factor (YIF1P), mRNA /cds=(116,997) /gb=NM_020470 /gi=9994168 /ug=Hs.406422 /len=1078	NM_020470	Hs.406422	NP_065203
3034	0.043451	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=NM_004568 /gi=28077084 /ug=Hs.41072 /len=1361	NM_004568	Hs.41072	NP_004559
3038	0.043451	golgi phosphoprotein 3 (coat-protein) (GOLPH3), mRNA /cds=(241,1137) /gb=NM_022130 /gi=20149665 /ug=Hs.18271 /len=2655	NM_022130	Hs.18271	NP_071413
3062	0.006234	myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), mRNA /cds=(115,630) /gb=NM_006471 /gi=5453739 /ug=Hs.180224 /len=944	NM_006471	Hs.180224	NP_006462
3065	0.041237	KIAA0433 protein (KIAA0433), mRNA /cds=(510,4241) /gb=NM_015216 /gi=7662117 /ug=Hs.26179 /len=5814	NM_015216	Hs.26179	NP_056031

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3070	0.041237	signal sequence receptor, beta (translocon-associated protein beta) (SSR2), mRNA /cds=(51,602) /gb=NM_003145 /gi=6552341 /ug=Hs.74564 /len=1093	NM_003145	Hs.74564	NP_003136
3071	0.006234	endothelin receptor type A (EDNRA), mRNA /cds=(485,1768) /gb=NM_001957 /gi=4503464 /ug=Hs.76252 /len=4105	NM_001957	Hs.76252	NP_001948
3072	0.017682	trichorhinophalangeal syndrome I (TRPS1), mRNA /cds=(639,4484) /gb=NM_014112 /gi=7657658 /ug=Hs.26102 /len=10011	NM_014112	Hs.26102	NP_054831
3073	0.003487	KIAA0174 gene product (KIAA0174), mRNA /cds=(64,1158) /gb=NM_014761 /gi=7661971 /ug=Hs.75824 /len=2348	NM_014761	Hs.75824	NP_055576
3076	0.033283	hypothetical protein FLJ20707 (FLJ20707), mRNA /cds=(83,2173) /gb=NM_032560 /gi=19923643 /ug=Hs.334657 /len=2794	NM_032560	Hs.334657	NP_115949
3108	0.011417	glycogen synthase 1 (muscle) (GYS1), mRNA /cds=(161,2374) /gb=NM_002103 /gi=4504232 /ug=Hs.772 /len=3531	NM_002103	Hs.772	NP_002094
3113	0.029809	phosphodiesterase 4D interacting protein (myomegalin) (PDE4DIP), mRNA /cds=(658,4056) /gb=NM_014644 /gi=11036643 /ug=Hs.265848 /len=5676	NM_014644	Hs.265848	NP_055459
3136	0.015649	splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(219,542) /gb=NM_006925 /gi=5902077 /ug=Hs.166975 /len=1865	NM_006925	Hs.166975	NP_008856
3137	0.025168	yp24c06.s1 Soares breast 3NbHBst cDNA clone IMAGE:188362 3' similar to gb:M10942_cds1 metallothionein-le gene mRNA sequence /clone=IMAGE:188362 /clone_end=3' /gb=H43642 /gi=919694 /ug=Hs.418241 /len=452	H43642	Hs.418241	
3138	0.001342	NCAG1 (NCAG1), mRNA /cds=(1477,5145) /gb=NM_032160 /gi=23943786 /ug=Hs.124673 /len=9528	NM_032160	Hs.124673	NP_115536
3139	0.045762	mRNA for KIAA0530 protein, partial cds. /cds=(1,4693) /gb=AB011102 /gi=3043583 /ug=Hs.173081 /len=6578	AB011102	Hs.173081	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3140	0.037084	DKFZp451H2115_r1 451 (synonym: hlcc1) spinal cord cDNA clone DKFZp451H2115 5', mRNA sequence /clone=DKFZp451H2115 /clone_end=5' /gb=AL589315 /gi=13243087 /ug=Hs.332004 /len=517	AL589315	Hs.332004	
3144	0.00104	solute carrier family 20 (phosphate transporter), member 1 (SLC20A1), mRNA /cds=(371,2410) /gb=NM_005415 /gi=7382462 /ug=Hs.78452 /len=3220	NM_005415	Hs.78452	NP_005406
3165	0.031506	SOCS box-containing WD protein SWiP-1 (WSB1), transcript variant 3, mRNA /cds=(317,1051) /gb=NM_134264 /gi=20143909 /ug=Hs.187991 /len=4243	NM_134264	Hs.187991	NP_599027
3166	0.037084	hypothetical protein FLJ13855 (FLJ13855), mRNA /cds=(328,1068) /gb=NM_023079 /gi=20149671 /ug=Hs.168232 /len=3053	NM_023079	Hs.168232	NP_075567
3172	0.006684	myocyte-specific enhancer factor 2A (MEF2A) gene, last coding exon, and complete cds	U49020		
3174	1.92E-04	lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA /cds=(69,476) /gb=NM_002305 /gi=6006015 /ug=Hs.382367 /len=526	NM_002305	Hs.382367	NP_002296
3175	0.018779	spermidine/spermine N1-acetyltransferase (SAT), mRNA /cds=(166,681) /gb=NM_002970 /gi=4506788 /ug=Hs.28491 /len=1060	NM_002970	Hs.28491	NP_002961
3180	0.045762	ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794 /ug=Hs.418650 /len=801	NM_002032	Hs.418650	NP_002023
3191	0.045762	hypothetical protein MGC14353 (MGC14353), mRNA /cds=(77,448) /gb=NM_032731 /gi=21362103 /ug=Hs.74346 /len=728	NM_032731	Hs.74346	NP_116120
3219	4.63E-04	actin, alpha, cardiac muscle (ACTC), mRNA /cds=(1,1134) /gb=NM_005159 /gi=10938011 /ug=Hs.118127 /len=1294	NM_005159	Hs.118127	NP_005150
3233	0.002995	uncharacterized hematopoietic stem/progenitor cells protein MDS027 (MDS027), mRNA /cds=(21,248) /gb=NM_018462 /gi=27544938 /ug=Hs.421654 /len=888	NM_018462	Hs.421654	NP_060932
3244	0.024901	hypothetical protein FLJ13352 (FLJ13352), mRNA /cds=(97,1053) /gb=NM_024592 /gi=13375784 /ug=Hs.22972 /len=2271	NM_024592	Hs.22972	NP_078868

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3254	0.035141	splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(156,821) /gb=NM_003016 /gi=4506898 /ug=Hs.73965 /len=1879	NM_003016	Hs.73965	NP_003007
3280	0.010023	RETROVIRUS-RELATED POLYPROTEIN	P11369		
3288	0.005811	cyclin G2 (CCNG2), mRNA /cds=(136,1170) /gb=NM_004354 /gi=4757935 /ug=Hs.79069 /len=2044	NM_004354	Hs.79069	NP_004345
3294	0.035141	NCK adaptor protein 1 (NCK1), mRNA /cds=(117,1250) /gb=NM_006153 /gi=20070226 /ug=Hs.54589 /len=1947	NM_006153	Hs.54589	NP_006144
3316	0.003487	glutathione S-transferase M3 (brain) (GSTM3), mRNA /cds=(311,988) /gb=NM_000849 /gi=23065551 /ug=Hs.2006 /len=1572	NM_000849	Hs.2006	NP_000840
3318	0.019933	endothelial protein C receptor	AB026584		
3327	0.048172	goliath protein (GP), mRNA /cds=(428,1258) /gb=NM_018434 /gi=20127393 /ug=Hs.155718 /len=1445	NM_018434	Hs.155718	NP_060904
3328	0.029809	retinoblastoma-like 2 (p130) (RBL2), mRNA /cds=(70,3489) /gb=NM_005611 /gi=21361291 /ug=Hs.79362 /len=4853	NM_005611	Hs.79362	NP_005602
3354	0.005038	ribosomal protein L23 (RPL23), mRNA /cds=(27,449) /gb=NM_000978 /gi=14591907 /ug=Hs.234518 /len=493	NM_000978	Hs.234518	NP_000969
3390	0.041237	phosphoribosyl pyrophosphate synthetase associated protein 2 (PRPSAP2), mRNA /cds=(212,1321) /gb=NM_002767 /gi=22538484 /ug=Hs.13339 /len=1890	NM_002767	Hs.13339	NP_002758
3405	0.022422	lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA /cds=(69,476) /gb=NM_002305 /gi=6006015 /ug=Hs.382367 /len=526	NM_002305	Hs.382367	NP_002296
3428	0.026643	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing) (ERCC3), mRNA /cds=(96,2444) /gb=NM_000122 /gi=4557562 /ug=Hs.77929 /len=2751	NM_000122	Hs.77929	NP_000113
3440	0.00767	TERF1 (TRF1)-interacting nuclear factor 2 (TINF2), mRNA /cds=(263,1327) /gb=NM_012461 /gi=6912715 /ug=Hs.7797 /len=2095	NM_012461	Hs.7797	NP_036593
3461	0.025168	ribosomal protein S3 (RPS3), mRNA /cds=(19,750) /gb=NM_001005 /gi=15718686 /ug=Hs.414990 /len=843	NM_001005	Hs.414990	NP_000996

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3512	0.043451	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
3520	0.016639	mRNA; cDNA DKFZp586F2423 (from clone DKFZp586F2423) /gb=AL080209 /gi=5262698 /ug=Hs.13659 /len=4254	AL080209	Hs.13659	
3538	0.035141	insulin-like growth factor binding protein 6 (IGFBP6), mRNA /cds=(54,776) /gb=NM_002178 /gi=11321592 /ug=Hs.274313 /len=952	NM_002178	Hs.274313	NP_002169
3539	0.037084	ubiquitin C (UBC), mRNA /cds=(136,2193) /gb=NM_021009 /gi=20149305 /ug=Hs.183704 /len=2309	NM_021009	Hs.183704	NP_066289
3548	0.011417	eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA /cds=(23,1360) /gb=NM_001568 /gi=4503520 /ug=Hs.106673 /len=1510	NM_001568	Hs.106673	NP_001559
3567	0.045762	FUS/TLS protein gene, alternatively spliced products, exons 1 through 15 and complete cds	AF071213		
3599	0.031506	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705	NM_006855	Hs.250696	NP_057839
3606	0.035141	nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs) (NOLA3), mRNA /cds=(98,292) /gb=NM_018648 /gi=15011920 /ug=Hs.14317 /len=556	NM_018648	Hs.14317	NP_061118
3607	0.028189	mitochondrion, complete genome	NC_001807		
3609	0.005038	mortality factor 4 like 1 (MORF4L1), mRNA /cds=(132,1103) /gb=NM_006791 /gi=5803101 /ug=Hs.6353 /len=1766	NM_006791	Hs.6353	NP_006782
3619	0.043451	cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 /len=802	NM_001861	Hs.433419	NP_001852
3641	1.56E-04	hypothetical protein CL25084 (CL25084), mRNA /cds=(132,1583) /gb=NM_015701 /gi=20070263 /ug=Hs.7100 /len=2412	NM_015701	Hs.7100	NP_056516
3642	0.001721	chromosome 1 open reading frame 22 (C1orf22), mRNA /cds=(54,2723) /gb=NM_025191 /gi=19923618 /ug=Hs.279951 /len=6298	NM_025191	Hs.279951	NP_079467

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3643	0.048172	chitinase 3-like 2 (CHI3L2), mRNA /cds=(36,1193) /gb=NM_004000 /gi=11993934 /ug=Hs.154138 /len=1418	NM_004000	Hs.154138	NP_003991
3733	0.048172	MAGEF1 protein (MAGEF1), mRNA /cds=(177,1103) /gb=NM_022149 /gi=11545891 /ug=Hs.306123 /len=1615	NM_022149	Hs.306123	NP_071432
3751	0.033283	S100 calcium binding protein A11 (calgizzarin) (S100A11), mRNA /cds=(121,438) /gb=NM_005620 /gi=5032056 /ug=Hs.417004 /len=595	NM_005620	Hs.417004	NP_005611
3763	0.01471	UI-E-EO1-aja-c-22-0-UI.s1 UI-E-EO1 cDNA clone UI-E-EO1-aja-c-22-0-UI 3', mRNA sequence /clone=UI-E-EO1-aja-c-22-0-UI /clone_end=3' /gb=BM680199 /gi=18990095 /ug=Hs.355581 /len=1071	BM680199	Hs.355581	
3787	0.008208	secretory leukocyte protease inhibitor (antileukoproteinase) (SLPI), mRNA /cds=(23,421) /gb=NM_003064 /gi=15834622 /ug=Hs.251754 /len=598	NM_003064	Hs.251754	NP_003055
3805	0.012975	hypothetical protein FLJ10350 (FLJ10350), mRNA /cds=(676,2340) /gb=NM_018067 /gi=21361780 /ug=Hs.177596 /len=2811	NM_018067	Hs.177596	NP_060537
3828	0.035141	osteoblast specific factor 2 (fasciclin I-like) (OSF-2), mRNA /cds=(12,2522) /gb=NM_006475 /gi=5453833 /ug=Hs.136348 /len=3213	NM_006475	Hs.136348	NP_006466
3830	0.018779	eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 /len=961	NM_001959	Hs.421608	NP_066944
3835	0.018779	NEL-like 2 (chicken) (NELL2), mRNA /cds=(97,2547) /gb=NM_006159 /gi=5453765 /ug=Hs.79389 /len=3198	NM_006159	Hs.79389	NP_006150
3840	0.019933	sorcin (SRI), mRNA /cds=(13,609) /gb=NM_003130 /gi=4507206 /ug=Hs.422340 /len=952	NM_003130	Hs.422340	NP_003121
3856	0.002566	translocase of inner mitochondrial membrane 10 (yeast) homolog (TIMM10)	NM_012456		NP_036588
3861	0.011417	basigin (BSG), mRNA /cds=(58,867) /gb=NM_001728 /gi=4502458 /ug=Hs.74631 /len=1638	NM_001728	Hs.74631	NP_001719
3872	0.028189	6-phosphogluconolactonase (PGLS), mRNA /cds=(18,794) /gb=NM_012088 /gi=6912585 /ug=Hs.100071 /len=1010	NM_012088	Hs.100071	NP_036220

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3888	0.041237	SAC2 suppressor of actin mutations 2-like (yeast) (SACM2L), transcript variant 1, mRNA /cds=(245,2416) /gb=NM_080564 /gi=18379336 /ug=Hs.169407 /len=2985	NM_080564	Hs.169407	NP_542131
3917	0.048172	ribosomal protein L30 (RPL30), mRNA /cds=(71,418) /gb=NM_000989 /gi=15812218 /ug=Hs.334807 /len=524	NM_000989	Hs.334807	NP_000980
3924	0.010701	ubiquitin specific protease 10 (USP10), mRNA /cds=(114,2510) /gb=NM_005153 /gi=24307888 /ug=Hs.78829 /len=3009	NM_005153	Hs.78829	NP_005144
3936	0.043451	hypothetical protein AF311304 (AF311304), mRNA /cds=(21,185) /gb=NM_031214 /gi=13654285 /ug=Hs.300624 /len=1138	NM_031214	Hs.300624	NP_112491
3942	0.010979	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) (SPTAN1), mRNA /cds=(103,7521) /gb=NM_003127 /gi=4507190 /ug=Hs.77196 /len=7787	NM_003127	Hs.77196	NP_003118
3954	0.002192	esophageal cancer related gene 4 protein (ECRG4), mRNA /cds=(109,555) /gb=NM_032411 /gi=14165275 /ug=Hs.43125 /len=772	NM_032411	Hs.43125	NP_115787
3970	0.043451	HSPC182 protein (HSPC182), mRNA /cds=(66,650) /gb=NM_014188 /gi=7661831 /ug=Hs.30026 /len=1059	NM_014188	Hs.30026	NP_054907
3976	0.01471	SFRS protein kinase 2 (SRPK2), mRNA /cds=(188,2248) /gb=NM_003138 /gi=4507220 /ug=Hs.78353 /len=3745	NM_003138	Hs.78353	NP_003129
3990	0.041237	hypothetical protein HSPC155 (HSPC155), mRNA /cds=(241,744) /gb=NM_016406 /gi=7705480 /ug=Hs.177507 /len=1137	NM_016406	Hs.177507	NP_057490
4000	0.028189	KIAA1156	AB032982		NP_055665
4004	0.001585	bromodomain containing 2 (BRD2), mRNA /cds=(1702,4107) /gb=NM_005104 /gi=12408641 /ug=Hs.75243 /len=4693	NM_005104	Hs.75243	NP_005095
4022	0.043451	MDS024 protein (MDS024), mRNA /cds=(65,838) /gb=NM_021820 /gi=11141892 /ug=Hs.425659 /len=2103	NM_021820	Hs.425659	NP_068592
4037	5.57E-04	coagulation factor VIII	AF062515		
4038	0.006234	multiple PDZ domain protein (MPDZ), mRNA /cds=(47,6175) /gb=NM_003829 /gi=4505230 /ug=Hs.169378 /len=6582	NM_003829	Hs.169378	NP_003820

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4046	2.04E-05	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa (POLR2C), transcript variant gamma, mRNA /cds=(58,885) /gb=NM_032940 /gi=14702170 /ug=Hs.79402 /len=1782	NM_032940	Hs.79402	NP_116558
4092	0.028189	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) (NDUFS3), mRNA /cds=(13,807) /gb=NM_004551 /gi=4758787 /ug=Hs.429506 /len=899	NM_004551	Hs.429506	NP_004542
4093	0.01471	coated vesicle membrane protein (RNP24), mRNA /cds=(24,629) /gb=NM_006815 /gi=21314646 /ug=Hs.75914 /len=2060	NM_006815	Hs.75914	NP_006806
4103	0.001459	protein kinase C, nu (PRKCN), mRNA /cds=(556,3228) /gb=NM_005813 /gi=6563384 /ug=Hs.143460 /len=5792	NM_005813	Hs.143460	NP_005804
4118	0.043451	HSPC154 protein (HSPC154), mRNA /cds=(200,946) /gb=NM_014177 /gi=7661809 /ug=Hs.7922 /len=1343	NM_014177	Hs.7922	NP_054896
4121	0.025168	natural killer cell enhancing factor (NKEFA)	L19184		NP_002565
4131	0.039115	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556	NM_021109	Hs.75968	NP_066932
4133	0.00767	vimentin (VIM), mRNA /cds=(123,1523) /gb=NM_003380 /gi=4507894 /ug=Hs.297753 /len=1851	NM_003380	Hs.297753	NP_000995
4152	0.035141	CG9469 gene product	AAF57414		
4159	0.048172	suppressor of Ty 3 (S. cerevisiae) (SUPT3H), mRNA /cds=(72,1025) /gb=NM_003599 /gi=4507308 /ug=Hs.304173 /len=1165	NM_003599	Hs.304173	NP_003590
4189	9.54E-04	fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4), transcript variant 2, mRNA /cds=(507,2642) /gb=NM_022977 /gi=12669908 /ug=Hs.81452 /len=5356	NM_022977	Hs.81452	NP_075266
4194	0.009383	peptidase D (PEPD), mRNA /cds=(17,1498) /gb=NM_000285 /gi=4557834 /ug=Hs.73947 /len=1888	NM_000285	Hs.73947	NP_000276
4200	0.012175	PTD013 protein (PTD013), mRNA /cds=(87,812) /gb=NM_015952 /gi=7706269 /ug=Hs.22679 /len=982	NM_015952	Hs.22679	NP_057036
4206	0.048172	ring finger protein 4 (RNF4), mRNA /cds=(271,843) /gb=NM_002938 /gi=4506560 /ug=Hs.66394 /len=2918	NM_002938	Hs.66394	NP_002929

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4213	0.035141	collagen, type V, alpha 2 (COL5A2), mRNA /cds=(158,4648) /gb=NM_000393 /gi=16554580 /ug=Hs.82985 /len=6217	NM_000393	Hs.82985	NP_000384
4223	1.27E-04	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 (SLC25A20), mitochondrial protein encoded by nuclear gene, mRNA /cds=(37,942) /gb=NM_000387 /gi=6006040 /ug=Hs.13845 /len=1219	NM_000387	Hs.13845	NP_000378
4267	0.029809	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein (ID1), mRNA /cds=(36,500) /gb=NM_002165 /gi=4504568 /ug=Hs.75424 /len=926	NM_002165	Hs.75424	NP_851998
4294	0.029809	hypothetical protein FLJ20729 (FLJ20729), mRNA /cds=(135,1547) /gb=NM_017953 /gi=20149642 /ug=Hs.5111 /len=2821	NM_017953	Hs.5111	NP_060423
4317	0.039115	accessory protein BAP31 (DXS1357E), mRNA /cds=(137,877) /gb=NM_005745 /gi=10047078 /ug=Hs.291904 /len=1314	NM_005745	Hs.291904	NP_005736
4339	0.043451	lamin B receptor (LBR), mRNA /cds=(76,1923) /gb=NM_002296 /gi=4504960 /ug=Hs.152931 /len=3714	NM_002296	Hs.152931	NP_002287
4364	0.039115	oxysterol binding protein-like 8 (OSBPL8), mRNA /cds=(481,3150) /gb=NM_020841 /gi=22035617 /ug=Hs.109694 /len=7239	NM_020841	Hs.109694	NP_065892
4369	0.035141	ribosomal protein L36 (RPL36), transcript variant 2, mRNA /cds=(153,470) /gb=NM_015414 /gi=16117793 /ug=Hs.433411 /len=545	NM_015414	Hs.433411	NP_378669
4390	0.013819	ataxia telangiectasia and Rad3 related (ATR), mRNA /cds=(106,8040) /gb=NM_001184 /gi=20143978 /ug=Hs.77613 /len=8265	NM_001184	Hs.77613	NP_001175
4407	0.045762	15 kDa selenoprotein (SEP15), mRNA /cds=(5,493) /gb=NM_004261 /gi=20127464 /ug=Hs.90606 /len=1519	NM_004261	Hs.90606	NP_004252
4419	0.029809	KIAA0742	AB018285		NP_060903
4425	0.005038	gene amplified in squamous cell carcinoma 1 (GASC1), mRNA /cds=(151,3321) /gb=NM_015061 /gi=24307986 /ug=Hs.149918 /len=4239	NM_015061	Hs.149918	NP_055876
4435	0.010701	clone IMAGE:3633225, mRNA /gb=BC012758 /gi=15706478 /ug=Hs.356377 /len=1914	BC012758	Hs.356377	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4440	0.031506	alcohol dehydrogenase 5 (class III), chi polypeptide (ADH5), mRNA /cds=(163,1287) /gb=NM_000671 /gi=11496890 /ug=Hs.78989 /len=2496	NM_000671	Hs.78989	NP_000662
4462	0.016639	collagen, type I, alpha 2 (COL1A2), mRNA /cds=(138,4238) /gb=NM_000089 /gi=21536289 /ug=Hs.179573 /len=5084	NM_000089	Hs.179573	NP_000080
4509	0.019933	likely ortholog of mouse deleted in polyposis 1 (DP1), mRNA /cds=(38,595) /gb=NM_005669 /gi=24307896 /ug=Hs.178112 /len=3000	NM_005669	Hs.178112	NP_005660
4513	0.029809	hepatitis B virus x interacting protein (HBXIP), mRNA /cds=(56,331) /gb=NM_006402 /gi=5454169 /ug=Hs.433355 /len=605	NM_006402	Hs.433355	NP_006393
4515	0.045762	cell recognition molecule CASPR3 (CASPR3), transcript variant 1, mRNA /cds=(408,3872) /gb=NM_033655 /gi=16306508 /ug=Hs.212839 /len=5017	NM_033655	Hs.212839	NP_387504
4530	0.00767	I factor (complement) (IF), mRNA /cds=(15,1766) /gb=NM_000204 /gi=4504578 /ug=Hs.36602 /len=1963	NM_000204	Hs.36602	NP_000195
4531	0.048172	erythrocyte membrane protein band 4.1-like 2 (EPB41L2), mRNA /cds=(45,3062) /gb=NM_001431 /gi=4503578 /ug=Hs.7857 /len=4336	NM_001431	Hs.7857	NP_001422
4536	0.035141	splicing factor, arginine/serine-rich 2, interacting protein (SFRS2IP), mRNA /cds=(1211,4657) /gb=NM_004719 /gi=4759171 /ug=Hs.51957 /len=5307	NM_004719	Hs.51957	NP_004710
4540	0.007162	decay accelerating factor for complement (CD55, Cromer blood group system) (DAF), mRNA /cds=(66,1211) /gb=NM_000574 /gi=10835142 /ug=Hs.1369 /len=2102	NM_000574	Hs.1369	NP_000565
4556	0.045762	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL), mRNA /cds=(52,2595) /gb=NM_002863 /gi=4506352 /ug=Hs.771 /len=2643	NM_002863	Hs.771	NP_002854
4584	0.008779	Rho-associated, coiled-coil containing protein kinase 1 (ROCK1), mRNA /cds=(1,4065) /gb=NM_005406 /gi=4885582 /ug=Hs.17820 /len=4065	NM_005406	Hs.17820	NP_005397
4654	0.041237	RNA helicase-related protein (RNAHP), mRNA /cds=(18,2147) /gb=NM_007372 /gi=11321631 /ug=Hs.8765 /len=3347	NM_007372	Hs.8765	NP_031398

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4672	0.017682	coronin, actin binding protein, 1C (CORO1C), mRNA /cds=(97,1521) /gb=NM_014325 /gi=27477119 /ug=Hs.17377 /len=3828	NM_014325	Hs.17377	NP_055140
4678	0.002372	hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA /cds=(49,2259) /gb=NM_000414 /gi=4504504 /ug=Hs.75441 /len=2593	NM_000414	Hs.75441	NP_000405
4693	0.002192	H3 histone, family 3B (H3.3B) (H3F3B), mRNA /cds=(118,528) /gb=NM_005324 /gi=21264598 /ug=Hs.180877 /len=1662	NM_005324	Hs.180877	NP_005315
4694	0.001459	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) (HIF1A), mRNA /cds=(265,2745) /gb=NM_001530 /gi=4504384 /ug=Hs.197540 /len=3933	NM_001530	Hs.197540	NP_851397
4703	0.013819	leukotriene A4 hydrolase (LTA4H), mRNA /cds=(69,1904) /gb=NM_000895 /gi=4505028 /ug=Hs.81118 /len=2060	NM_000895	Hs.81118	NP_000886
4720	0.026643	heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA /cds=(91,1992) /gb=NM_005826 /gi=14141188 /ug=Hs.15265 /len=2663	NM_005826	Hs.15265	NP_005817
4724	0.035141	Niemann-Pick disease, type C1 (NPC1), mRNA /cds=(124,3960) /gb=NM_000271 /gi=4557802 /ug=Hs.76918 /len=4673	NM_000271	Hs.76918	NP_000262
4736	0.003758	E74-like factor 1 (ets domain transcription factor) (ELF1), mRNA /cds=(256,2115) /gb=NM_172373 /gi=27363483 /ug=Hs.154365 /len=3526	NM_172373	Hs.154365	NP_758961
4741	0.033283	hypothetical protein MGC21981 (MGC21981), mRNA /cds=(66,764) /gb=NM_153267 /gi=23397567 /ug=Hs.131987 /len=1727	NM_153267	Hs.131987	NP_694999
4758	0.026643	inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA /cds=(86,1366) /gb=NM_002192 /gi=4504698 /ug=Hs.727 /len=1840	NM_002192	Hs.727	NP_002183
4769	0.018779	mitochondrial ribosomal protein L37 (MRPL37), nuclear gene encoding mitochondrial protein, mRNA /cds=(78,1349) /gb=NM_016491 /gi=22547133 /ug=Hs.4209 /len=1511	NM_016491	Hs.4209	NP_057575
4774	0.019933	ribosomal protein S19 (RPS19), mRNA /cds=(70,507) /gb=NM_001022 /gi=14591914 /ug=Hs.298262 /len=569	NM_001022	Hs.298262	NP_001013
4778	0.026643	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4782	0.01471	CDC-like kinase1 (CLK1), mRNA /cds=(156,1610) /gb=NM_004071 /gi=4758007 /ug=Hs.2083 /len=1834	NM_004071	Hs.2083	NP_004062
4794	0.012975	mitochondrion, complete genome	NC_001807		
4798	0.022422	Rho-associated, coiled-coil containing protein kinase 2 (ROCK2), mRNA /cds=(455,4621) /gb=NM_004850 /gi=6633807 /ug=Hs.58617 /len=6409	NM_004850	Hs.58617	NP_004841
4805	0.001234	high-mobility group box 1 (HMGB1), mRNA /cds=(77,724) /gb=NM_002128 /gi=20149538 /ug=Hs.6727 /len=1207	NM_002128	Hs.6727	NP_002119
4810	0.041237	mRNA; cDNA DKFZp727I051 (from clone DKFZp727I051); partial cds /cds=(1,2099) /gb=AL117478 /gi=5911952 /ug=Hs.239370 /len=2480	AL117478	Hs.239370	NP_056412
4814	0.012975	ribosomal protein L10a (RPL10A), mRNA /cds=(16,669) /gb=NM_007104 /gi=15431287 /ug=Hs.425293 /len=700	NM_007104	Hs.425293	NP_009035
4819	0.015649	ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500	NM_000991	Hs.356371	NP_000982
4821	0.01471	eukaryotic translation termination factor 1 (ETF1), mRNA /cds=(136,1449) /gb=NM_004730 /gi=4759033 /ug=Hs.77324 /len=3653	NM_004730	Hs.77324	NP_004721
4823	0.035141	SH3-domain GRB2-like endophilin B2 (SH3GLB2), mRNA /cds=(147,1334) /gb=NM_020145 /gi=24431995 /ug=Hs.30002 /len=2039	NM_020145	Hs.30002	NP_064530
4837	0.041237	UI-H-BW1-amj-g-07-0-UI.s1 NCI_CGAP_Sub7 cDNA clone IMAGE:3070261 3', mRNA sequence /clone=IMAGE:3070261 /clone_end=3' /gb=BF513214 /gi=11598393 /ug=Hs.445888 /len=620	BF513214	Hs.445888	
4848	0.005811	aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 2, mRNA /cds=(61,7308) /gb=NM_013227 /gi=6995993 /ug=Hs.2159 /len=7434	NM_013227	Hs.2159	NP_037359
4863	0.025168	FLJ14819 fis, clone OVARC1000241, moderately similar to HYPOXIA-INDUCIBLE FACTOR 1 ALPHA	AK027725		NP_690009
4874	0.016639	ankyrin repeat domain 10 (ANKRD10), mRNA /cds=(136,1398) /gb=NM_017664 /gi=8923103 /ug=Hs.172572 /len=2509	NM_017664	Hs.172572	NP_060134

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4877	0.023762	chromosome 20 open reading frame 31 (C20orf31), mRNA /cds=(83,1819) /gb=NM_018217 /gi=8922666 /ug=Hs.93871 /len=1885	NM_018217	Hs.93871	NP_060687
4878	0.009383	ribosomal protein L35a (RPL35A), mRNA /cds=(74,406) /gb=NM_000996 /gi=16117790 /ug=Hs.288544 /len=511	NM_000996	Hs.288544	NP_000987
4880	0.035141	cDNA FLJ12776 fis, clone NT2RP2001678. /gb=AK022838 /gi=10434465 /ug=Hs.372558 /len=2629	AK022838	Hs.372558	
4884	0.006293	geranylgeranyl diphosphate synthase 1 (GGPS1), mRNA /cds=(233,1135) /gb=NM_004837 /gi=21359876 /ug=Hs.55498 /len=1489	NM_004837	Hs.55498	NP_004828
4886	0.026643	proteasome (prosome, macropain) subunit, beta type, 4 (PSMB4), mRNA /cds=(24,818) /gb=NM_002796 /gi=22538466 /ug=Hs.89545 /len=925	NM_002796	Hs.89545	NP_002787
4912	0.037157	ATP synthase, H transporting, mitochondrial F0 complex, subunit g (ATP5L), mRNA /cds=(60,371) /gb=NM_006476 /gi=21359881 /ug=Hs.107476 /len=580	NM_006476	Hs.107476	NP_006467
4915	0.004357	hypothetical protein FLJ13149 (FLJ13149), mRNA /cds=(291,2585) /gb=NM_021826 /gi=11141902 /ug=Hs.112188 /len=2836	NM_021826	Hs.112188	NP_068598
4916	0.015649	collagen, type X, alpha 1(Schmid metaphyseal chondrodysplasia) (COL10A1), mRNA /cds=(97,2139) /gb=NM_000493 /gi=18105031 /ug=Hs.179729 /len=3285	NM_000493	Hs.179729	NP_000484
4919	0.001459	KIAA0436 mRNA, partial cds. /cds=(1,2070) /gb=AB007896 /gi=2662152 /ug=Hs.110 /len=4661	AB007896	Hs.110	
4921	0.025168	cDNA FLJ10423 fis, clone NT2RP1000259. /gb=AK001285 /gi=7022444 /ug=Hs.106909 /len=1837	AK001285	Hs.106909	
4925	0.012175	tm68a09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2163256 3', mRNA sequence /clone=IMAGE:2163256 /clone_end=3' /gb=AI498805 /gi=4390787 /ug=Hs.436349 /len=460	AI498805	Hs.436349	
4926	0.00767	nuclear receptor coactivator 1 (NCOA1), transcript variant 2, mRNA /cds=(202,4401) /gb=NM_147223 /gi=22538456 /ug=Hs.74002 /len=4721	NM_147223	Hs.74002	NP_671766

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4942	0.018779	AF034176 mRNA (Tripodis and Ragoussis) cDNA clone ntcon5 contig /gb=AF034176 /gi=2707738 /ug=Hs.188882 /len=7232	AF034176	Hs.188882	
4944	0.005412	hypothetical protein FLJ20452 (FLJ20452), mRNA /cds=(15,614) /gb=NM_017828 /gi=21361660 /ug=Hs.351327 /len=1948	NM_017828	Hs.351327	NP_060298
4945	0.012975	eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa (EIF3S5), mRNA /cds=(7,1080) /gb=NM_003754 /gi=4503518 /ug=Hs.7811 /len=1231	NM_003754	Hs.7811	NP_003745
4946	0.001661	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_079425	Hs.77385	NP_524149
4950	0.045762	mRNA for KIAA1865 protein, partial cds. /cds=(622,2793) /gb=AB058768 /gi=14017946 /ug=Hs.179260 /len=3641	AB058768	Hs.179260	
4956	0.018779	hypothetical protein FLJ20671 (FLJ20671), mRNA /cds=(43,465) /gb=NM_017924 /gi=19923511 /ug=Hs.180201 /len=2855	NM_017924	Hs.180201	NP_060394
4957	0.012975	TcD37 (HTCD37), mRNA /cds=(137,1498) /gb=NM_021222 /gi=24308262 /ug=Hs.78524 /len=2995	NM_021222	Hs.78524	NP_067045
4958	0.016639	cDNA FLJ10235 fis, clone HEMBB1000339. /gb=AK001097 /gi=7022149 /ug=Hs.406774 /len=2530	AK001097	Hs.406774	
4962	0.027396	mRNA for KIAA1320 protein, partial cds. /cds=(2051,3754) /gb=AB037741 /gi=7243020 /ug=Hs.117414 /len=5321	AB037741	Hs.117414	
4970	0.022422	decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=NM_001920 /gi=19743844 /ug=Hs.433989 /len=1751	NM_001920	Hs.433989	NP_598014
4972	0.048172	HSPC092	AF161355		NP_055238
4983	0.035151	F-box and leucine-rich repeat protein 3A (FBXL3A), mRNA /cds=(298,1584) /gb=NM_012158 /gi=16306583 /ug=Hs.7540 /len=3489	NM_012158	Hs.7540	NP_036290
4986	0.003487	adrenomedullin (ADM), mRNA /cds=(157,714) /gb=NM_001124 /gi=4501944 /ug=Hs.394 /len=1449	NM_001124	Hs.394	NP_001115
4988	0.010701	translocase of outer mitochondrial membrane 70 A (yeast) (TOMM70A), mRNA /cds=(92,1918) /gb=NM_014820 /gi=7662672 /ug=Hs.21198 /len=4017	NM_014820	Hs.21198	NP_055635

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4989	0.045762	chloride intracellular channel 5 (CLIC5), mRNA /cds=(298,1053) /gb=NM_016929 /gi=8393146 /ug=Hs.283021 /len=2380	NM_016929	Hs.283021	NP_058625
4992	0.005412	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI), mRNA /cds=(1,915) /gb=NM_006287 /gi=6715569 /ug=Hs.170279 /len=915	NM_006287	Hs.170279	NP_006278
4994	0.007162	Nedd4 binding protein 2 (N4BP2), mRNA /cds=(339,5600) /gb=NM_018177 /gi=20357506 /ug=Hs.18685 /len=6760	NM_018177	Hs.18685	NP_060647
5005	0.029809	ankyrin repeat and SOCS box-containing 1 (ASB1), mRNA /cds=(87,1094) /gb=NM_016114 /gi=22208961 /ug=Hs.153489 /len=6798	NM_016114	Hs.153489	NP_057198
5011	0.001721	ALL1 fused gene from 5q31 (AF5Q31), mRNA /cds=(338,3829) /gb=NM_014423 /gi=7656878 /ug=Hs.231967 /len=4235	NM_014423	Hs.231967	NP_055238
5016	0.025168	ribosomal protein L17 (RPL17), mRNA /cds=(287,841) /gb=NM_000985 /gi=14591906 /ug=Hs.82202 /len=898	NM_000985	Hs.82202	NP_000976
5060	5.57E-04	HIF-1 responsive RTP801 (RTP801), mRNA /cds=(198,896) /gb=NM_019058 /gi=9506686 /ug=Hs.111244 /len=1760	NM_019058	Hs.111244	NP_061931
5061	0.016639	wc09c01.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:2314656 3' similar to gb:J05016 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR mRNA sequence /clone=IMAGE:2314656 /clone_end=3' /gb=AI674177 /gi=4874657 /ug=Hs.200089 /len=526	AI674177	Hs.200089	
5069	0.009383	hsp70-interacting protein (HSPBP1), mRNA /cds=(312,1400) /gb=NM_012267 /gi=21361406 /ug=Hs.53066 /len=1795	NM_012267	Hs.53066	NP_036399
5090	0.033283	U3 small nuclear RNA gene	M14061		
5094	0.006234	sterol regulatory element binding transcription factor 2 (SREBF2), mRNA /cds=(170,3595) /gb=NM_004599 /gi=27477112 /ug=Hs.108689 /len=4325	NM_004599	Hs.108689	NP_004590
5102	2.35E-04	cofilin 1 (non-muscle) (CFL1), mRNA /cds=(52,552) /gb=NM_005507 /gi=5031634 /ug=Hs.180370 /len=1059	NM_005507	Hs.180370	NP_005498

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5105	0.017682	hypothetical protein FLJ20312 (FLJ20312), mRNA /cds=(384,803) /gb=NM_017761 /gi=20127576 /ug=Hs.7862 /len=2382	NM_017761	Hs.7862	NP_060231
5108	0.005412	calponin 2 (CNN2), mRNA /cds=(28,957) /gb=NM_004368 /gi=4758017 /ug=Hs.169718 /len=2122	NM_004368	Hs.169718	NP_004359
5111	0.00767	chromosome 14 open reading frame 94 (C14orf94), mRNA /cds=(211,1302) /gb=NM_017815 /gi=8923395 /ug=Hs.8886 /len=1618	NM_017815	Hs.8886	NP_060285
5155	0.043451	phosphoglycerate kinase 1 (PGK1), mRNA /cds=(70,1323) /gb=NM_000291 /gi=22095338 /ug=Hs.78771 /len=2338	NM_000291	Hs.78771	NP_000282
5156	0.006684	myosin regulatory light chain (MLC-B), mRNA /cds=(117,635) /gb=NM_033546 /gi=15809015 /ug=Hs.233936 /len=967	NM_033546	Hs.233936	NP_291024
5161	0.018779	basic transcription factor 3 (BTF3), mRNA /cds=(240,728) /gb=NM_001207 /gi=20070129 /ug=Hs.101025 /len=952	NM_001207	Hs.101025	NP_001198
5187	0.012175	zinc finger protein 281 (ZNF281), mRNA /cds=(24,2711) /gb=NM_012482 /gi=6912751 /ug=Hs.59757 /len=3029	NM_012482	Hs.59757	NP_036614
5192	0.043451	mRNA for KIAA0232 protein, partial cds. /cds=(435,4643) /gb=D86985 /gi=20521849 /ug=Hs.79276 /len=7840	D86985	Hs.79276	
5195	0.003233	angiopoietin-like 4 (ANGPTL4), transcript variant 1, mRNA /cds=(196,1416) /gb=NM_139314 /gi=21536397 /ug=Hs.9613 /len=1967	NM_139314	Hs.9613	NP_647475
5204	0.039115	stathmin-like 3 (STMN3), mRNA /cds=(83,625) /gb=NM_015894 /gi=14670374 /ug=Hs.285753 /len=2255	NM_015894	Hs.285753	NP_056978
5205	0.043451	mRNA for KIAA1458 protein, partial cds. /cds=(22,1860) /gb=AB040891 /gi=7959176 /ug=Hs.27263 /len=5843	AB040891	Hs.27263	
5206	0.017682	CAAX box 1 (CXX1), mRNA /cds=(335,964) /gb=NM_003928 /gi=4503180 /ug=Hs.250708 /len=1209	NM_003928	Hs.250708	NP_003919
5234	0.031506	deiodinase, iodothyronine, type II (DIO2), transcript variant 1, mRNA /cds=(707,1528) /gb=NM_013989 /gi=7549802 /ug=Hs.154424 /len=6735	NM_013989	Hs.154424	NP_054644
5235	0.012975	major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA /cds=(63,863) /gb=NM_002124 /gi=4504410 /ug=Hs.375570 /len=1182	NM_002124	Hs.375570	NP_002115
5249	0.026643	Escherichia coli K-12 MG1655 section 343 of 400 of the complete genome	AE000453		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5250	0.010023	SFRS protein kinase 1 (SRPK1), mRNA /cds=(10,1974) /gb=NM_003137 /gi=15834623 /ug=Hs.75761 /len=4244	NM_003137	Hs.75761	NP_003128
5261	0.031506	replication factor C (activator 1) 4, 37kDa (RFC4), mRNA /cds=(284,1375) /gb=NM_002916 /gi=4506490 /ug=Hs.35120 /len=1446	NM_002916	Hs.35120	NP_002907
5264	0.005412	small GTP-binding protein RAB1A	AF226873		NP_033022
5283	0.037084	transforming, acidic coiled-coil containing protein 2 (TACC2), mRNA /cds=(87,3167) /gb=NM_006997 /gi=11119413 /ug=Hs.272023 /len=3686	NM_006997	Hs.272023	NP_008928
5287	0.01471	hypothetical protein FLJ30945 fis, clone FEBRA2007613	AK055507		NP_071911
5330	0.001234	discs, large 7 (Drosophila) (DLG7), mRNA /cds=(218,2758) /gb=NM_014750 /gi=21361644 /ug=Hs.77695 /len=2979	NM_014750	Hs.77695	NP_055565
5332	0.041237	clone IMAGE:5262128, mRNA, partial cds /cds=(1,1409) /gb=BC035036 /gi=23271542 /ug=Hs.356247 /len=4728	BC035036	Hs.356247	
5386	0.037084	ATPase; H transporting, lysosomal 9kDa, V0 subunit e (ATP6V0E), mRNA /cds=(76,321) /gb=NM_003945 /gi=19913435 /ug=Hs.415629 /len=849	NM_003945	Hs.415629	NP_003936
5391	0.005412	palmdelphin (PALMD), mRNA /cds=(286,1941) /gb=NM_017734 /gi=16306484 /ug=Hs.14606 /len=2581	NM_017734	Hs.14606	NP_060204
5411	0.045762	DKFZp566J2446 (from clone DKFZp566J2446)	AL050082		NP_008944
5412	0.026643	SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA /cds=(373,1902) /gb=NM_000346 /gi=4557852 /ug=Hs.2316 /len=3936	NM_000346	Hs.2316	NP_000337
5419	0.045321	ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1 (ATP5G1), mRNA /cds=(120,530) /gb=NM_005175 /gi=4885080 /ug=Hs.80986 /len=631	NM_005175	Hs.80986	NP_005166
5420	0.001459	matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=NM_002381 /gi=13518040 /ug=Hs.278461 /len=2599	NM_002381	Hs.278461	NP_002372
5432	0.025168	zinc finger protein 202 (ZNF202), mRNA /cds=(11,1957) /gb=NM_003455 /gi=10835040 /ug=Hs.9443 /len=4053	NM_003455	Hs.9443	NP_003446
5433	0.017682	actin related protein 2/3 complex, subunit 5, 16kDa (ARPC5), mRNA /cds=(192,647) /gb=NM_005717 /gi=23238212 /ug=Hs.82425 /len=2000	NM_005717	Hs.82425	NP_005708

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5438	0.010023	mitochondrion, complete genome	NC_001807		
5445	0.005051	hypothetical protein FLJ20312 (FLJ20312), mRNA /cds=(384,803) /gb=NM_017761 /gi=20127576 /ug=Hs.7862 /len=2382	NM_017761	Hs.7862	NP_060231
5448	0.037084	eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA /cds=(16,1239) /gb=NM_001967 /gi=9945313 /ug=Hs.173912 /len=1864	NM_001967	Hs.173912	NP_001958
5449	0.004357	mRNA; cDNA DKFZp667D2123 (from clone DKFZp667D2123) /gb=AL832786 /gi=21733368 /ug=Hs.283643 /len=3000	AL832786	Hs.283643	
5451	0.035141	tumor protein, translationally-controlled 1 (TPT1), mRNA /cds=(95,613) /gb=NM_003295 /gi=4507668 /ug=Hs.401448 /len=830	NM_003295	Hs.401448	NP_003286
5476	0.004687	meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA /cds=(315,2729) /gb=NM_005930 /gi=5174560 /ug=Hs.117242 /len=3676	NM_005930	Hs.117242	NP_005921
5477	0.002372	lectin, galactoside-binding, soluble, 3 (galectin 3) (LGALS3), mRNA /cds=(19,771) /gb=NM_002306 /gi=4504982 /ug=Hs.621 /len=914	NM_002306	Hs.621	NP_002297
5482	0.023762	proliferating cell nuclear antigen (PCNA), mRNA /cds=(119,904) /gb=NM_002592 /gi=4505640 /ug=Hs.78996 /len=1231	NM_002592	Hs.78996	NP_002583
5497	0.033283	zinc finger, DHHC domain containing 4 (ZDHHC4), mRNA /cds=(222,1256) /gb=NM_018106 /gi=21361700 /ug=Hs.5268 /len=1704	NM_018106	Hs.5268	NP_060576
5498	0.045762	polymerase (RNA) II (DNA directed) polypeptide G (POLR2G), mRNA /cds=(107,625) /gb=NM_002696 /gi=4505946 /ug=Hs.14839 /len=828	NM_002696	Hs.14839	NP_002687
5499	0.041237	adaptor-related protein complex 2, sigma 1 subunit (AP2S1), transcript variant AP17, mRNA /cds=(71,499) /gb=NM_004069 /gi=11038644 /ug=Hs.119591 /len=781	NM_004069	Hs.119591	NP_067586
5509	0.019933	brain protein 44-like (BRP44L), mRNA /cds=(123,452) /gb=NM_016098 /gi=7706368 /ug=Hs.108725 /len=988	NM_016098	Hs.108725	NP_057182
5511	0.010023	cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 /len=802	NM_001861	Hs.433419	NP_001852

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5514	0.00767	ribosomal protein L4 (RPL4), mRNA /cds=(57,1340) /gb=NM_000968 /gi=16579884 /ug=Hs.286 /len=1449	NM_000968	Hs.286	NP_000959
5517	0.026643	Hypothetical protein (cDNA FLJ20702 fis, clone KAIA2174)	AK000709		
5550	0.033283	fusion, derived from t(12;16) malignant liposarcoma (FUS), mRNA /cds=(79,1659) /gb=NM_004960 /gi=4826733 /ug=Hs.99969 /len=1824	NM_004960	Hs.99969	NP_004951
5551	0.037084	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit (HADHA), mRNA /cds=(35,2326) /gb=NM_000182 /gi=20127407 /ug=Hs.75860 /len=2972	NM_000182	Hs.75860	NP_000173
5584	0.019933	regulator of nonsense transcripts 1 (RENT1), mRNA /cds=(232,3588) /gb=NM_002911 /gi=18375672 /ug=Hs.12719 /len=5300	NM_002911	Hs.12719	NP_002902
5590	0.026643	eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), mRNA /cds=(15,752) /gb=NM_004846 /gi=4757701 /ug=Hs.19122 /len=974	NM_004846	Hs.19122	NP_004837
5640	0.012175	nonhistone protein HMG1	M21683		
5644	0.029809	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700	NM_002211	Hs.287797	NP_596867
5671	0.006684	EPC-1 (=M76979 PEDF;U29953;M90493)	U57446		
5672	0.004357	clone IMAGE:5265581, mRNA /gb=BC035165 /gi=23272508 /ug=Hs.400548 /len=2237	BC035165	Hs.400548	
5752	0.013819	F-box and leucine-rich repeat protein 7 (FBXL7), mRNA /cds=(482,1957) /gb=NM_012304 /gi=21071079 /ug=Hs.76798 /len=4562	NM_012304	Hs.76798	NP_036436
5770	0.023762	APG12 autophagy 12-like (S. cerevisiae), DKFZp761A0411 (from clone DKFZp761A0411) mRNA; cDNA /cds=UNKNOWN /gb=AL161968 /gi=7328057 /ug=Hs.264482 /len=3285	AL161968	Hs.264482	NP_004698
5789	0.015649	ribosomal protein L31 (RPL31), mRNA /cds=(28,405) /gb=NM_000993 /gi=15812219 /ug=Hs.184014 /len=442	NM_000993	Hs.184014	NP_000984

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5814	0.015649	ribosomal protein L36a-like (RPL36AL), mRNA /cds=(95,415) /gb=NM_001001 /gi=16306559 /ug=Hs.419465 /len=537	NM_001001	Hs.419465	NP_000992
5821	0.028189	ribosomal protein L11 (RPL11), mRNA /cds=(21,557) /gb=NM_000975 /gi=15431289 /ug=Hs.388664 /len=609	NM_000975	Hs.388664	NP_000966
5824	0.033283	activated RNA polymerase II transcription cofactor 4 (PC4), mRNA /cds=(57,440) /gb=NM_006713 /gi=19923783 /ug=Hs.349506 /len=1336	NM_006713	Hs.349506	NP_006704
5827	0.010701	PHKB gene (exon 25)	X84930		
5870	0.035141	Similar to cyclin K, clone MGC:9113 IMAGE:3907416, mRNA, complete cds /cds=(110,1174) /gb=BC015935 /gi=16198507 /ug=Hs.375192 /len=1925	BC015935	Hs.375192	
5899	0.006684	Fas (TNFRSF6) associated factor 1 (FAF1), transcript variant 1, mRNA /cds=(454,2406) /gb=NM_007051 /gi=19528653 /ug=Hs.25821 /len=2610	NM_007051	Hs.25821	NP_572051
5918	0.026643	Mus musculus mitochondrion, complete genome	NC_001569		
5928	0.021147	ubiquitin-conjugating enzyme E2B (RAD6 (UBE2B), mRNA /cds=(422,880) /gb=NM_003337 /gi=4507770 /ug=Hs.811 /len=2591	NM_003337	Hs.811	NP_003328
5934	0.006762	enthoprotin (ENTH), mRNA /cds=(102,1979) /gb=NM_014666 /gi=7661967 /ug=Hs.132853 /len=3336	NM_014666	Hs.132853	NP_055481
5937	0.045762	mitogen-activated protein kinase 9 (MAPK9), transcript variant 3, mRNA /cds=(50,1198) /gb=NM_139069 /gi=21237741 /ug=Hs.246857 /len=1947	NM_139069	Hs.246857	NP_620709
5938	0.013819	chaperonin containing TCP1, subunit 3 (gamma) (CCT3), mRNA /cds=(1,1635) /gb=NM_005998 /gi=5174726 /ug=Hs.1708 /len=1901	NM_005998	Hs.1708	NP_005989
5939	0.012175	BTA1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 S. cerevisiae) (BTA1), mRNA /cds=(118,5667) /gb=NM_003972 /gi=27477069 /ug=Hs.180930 /len=6345	NM_003972	Hs.180930	NP_003963
5959	0.013819	germline T-cell receptor beta chain	U66061		
5971	0.008779	UI-E-C11-abg-f-09-0-UI.r1 UI-E-C11 cDNA clone UI-E-C11-abg-f-09-0-UI 5', mRNA sequence /clone=UI-E-C11-abg-f-09-0-UI /clone_end=5' /gb=BM691540 /gi=19004798 /ug=Hs.172047 /len=1039	BM691540	Hs.172047	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5974	0.015649	KIAA0266 gene product (KIAA0266), mRNA /cds=(734,3034) /gb=NM_021645 /gi=11063982 /ug=Hs.127376 /len=5585	NM_021645	Hs.127376	NP_067677
5976	0.045762	ox06a01.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:1655496 3' similar to gb:M86849 GAP JUNCTION BETA-2 PROTEIN mRNA sequence /clone=IMAGE:1655496 /clone_end=3' /gb=AI033469 /gi=3254422 /ug=Hs.386279 /len=551	AI033469	Hs.386279	
6004	0.048172	UDP-glucose pyrophosphorylase 2 (UGP2), mRNA /cds=(85,1611) /gb=NM_006759 /gi=13027637 /ug=Hs.77837 /len=1832	NM_006759	Hs.77837	NP_006750
6006	0.018779	ribosomal protein L23a (RPL23A), mRNA /cds=(22,492) /gb=NM_000984 /gi=17105393 /ug=Hs.419463 /len=546	NM_000984	Hs.419463	NP_000975
6009	4.63E-04	methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,2329) /gb=NM_000255 /gi=4557766 /ug=Hs.155212 /len=2798	NM_000255	Hs.155212	NP_000246
6027	0.025168	mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA /cds=(182,1093) /gb=NM_005924 /gi=21396478 /ug=Hs.77858 /len=2284	NM_005924	Hs.77858	NP_005915
6028	0.043451	protein-tyrosine kinase, trkB	X75958		NP_006171
6034	0.026643	NRAS-related gene (D1S155E), mRNA /cds=(428,2824) /gb=NM_007158 /gi=20070240 /ug=Hs.69855 /len=4076	NM_007158	Hs.69855	NP_009089
6037	0.006234	splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(156,821) /gb=NM_003016 /gi=4506898 /ug=Hs.73965 /len=1879	NM_003016	Hs.73965	NP_003007
6042	0.007162	laminin, gamma 1 (formerly LAMB2) (LAMC1), mRNA /cds=(300,5129) /gb=NM_002293 /gi=9845497 /ug=Hs.432855 /len=7923	NM_002293	Hs.432855	NP_002284
6068	0.048172	mitochondrial ribosomal protein L27 (MRPL27), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA /cds=(32,316) /gb=NM_148571 /gi=22547130 /ug=Hs.7736 /len=2472	NM_148571	Hs.7736	NP_683412

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6069	0.022422	stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4 (SERP1), mRNA /cds=(316,516) /gb=NM_014445 /gi=19923408 /ug=Hs.76698 /len=2488	NM_014445	Hs.76698	NP_055260
6083	0.033283	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA /cds=(9,536) /gb=NM_002495 /gi=4505368 /ug=Hs.10758 /len=668	NM_002495	Hs.10758	NP_002486
6106	0.009383	EST (ym17h04.s1 clone 48282 3')	H11657		
6139	0.015649	cofilin 1 (non-muscle) (CFL1), mRNA /cds=(52,552) /gb=NM_005507 /gi=5031634 /ug=Hs.180370 /len=1059	NM_005507	Hs.180370	NP_005498
6159	0.045762	general transCRiption factor 2-I (GTF2I)	AF038968		NP_127496
6182	0.028189	signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), mRNA /cds=(57,614) /gb=NM_007107 /gi=6005883 /ug=Hs.28707 /len=3061	NM_007107	Hs.28707	NP_009038
6185	0.001721	chloride intracellular channel 4 (CLIC4), mRNA /cds=(198,959) /gb=NM_013943 /gi=7330334 /ug=Hs.25035 /len=4318	NM_013943	Hs.25035	NP_039234
6205	0.039115	jumping translocation breakpoint (JTB), mRNA /cds=(433,873) /gb=NM_006694 /gi=5729888 /ug=Hs.6396 /len=1040	NM_006694	Hs.6396	NP_006685
6262	0.018779	UDP-glucose ceramide glucosyltransferase-like 2 (UGCG2), mRNA /cds=(72,4622) /gb=NM_020121 /gi=11386200 /ug=Hs.22983 /len=4848	NM_020121	Hs.22983	NP_064506
6322	0.006684	ubiquitin specific protease 9 (USP9Y)	XM_000563		
6341	0.005811	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 (ADAMTS1), mRNA /cds=(294,3146) /gb=NM_006988 /gi=11038653 /ug=Hs.8230 /len=4459	NM_006988	Hs.8230	NP_008919
6403	0.004687	glyceronephosphate O-acyltransferase (GNPAT), mRNA /cds=(158,2200) /gb=NM_014236 /gi=7657133 /ug=Hs.12482 /len=2470	NM_014236	Hs.12482	NP_055051
6428	0.028189	serologically defined colon cancer antigen 1 (SDCCAG1), mRNA /cds=(183,1271) /gb=NM_004713 /gi=4759077 /ug=Hs.388584 /len=2078	NM_004713	Hs.388584	NP_004704
6429	0.033283	ubiquitin A-52 residue ribosomal protein fusion product 1 (UBA52), mRNA /cds=(39,425) /gb=NM_003333 /gi=15451941 /ug=Hs.5308 /len=515	NM_003333	Hs.5308	NP_003324

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6442	0.025168	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), mRNA /cds=(115,1677) /gb=NM_004566 /gi=4758899 /ug=Hs.195471 /len=4322	NM_004566	Hs.195471	NP_004557
6529	0.00767	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA /cds=(95,1048) /gb=NM_020529 /gi=10092618 /ug=Hs.81328 /len=1550	NM_020529	Hs.81328	NP_065390
6543	0.045762	general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), mRNA /cds=(161,1807) /gb=NM_005316 /gi=19923304 /ug=Hs.89578 /len=2989	NM_005316	Hs.89578	NP_005307
6565	0.002995	PTK9 protein tyrosine kinase 9 (PTK9), mRNA /cds=(61,1113) /gb=NM_002822 /gi=4506274 /ug=Hs.82643 /len=3000	NM_002822	Hs.82643	NP_002813
6566	0.019933	RAB11A, member RAS oncogene family (RAB11A), mRNA /cds=(104,754) /gb=NM_004663 /gi=20149549 /ug=Hs.75618 /len=2474	NM_004663	Hs.75618	NP_004654
6570	0.002773	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), mRNA /cds=(25,753) /gb=NM_003574 /gi=20070155 /ug=Hs.9006 /len=1390	NM_003574	Hs.9006	NP_003565
6577	0.012175	ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986	NM_004152	Hs.281960	NP_004143
6583	0.045762	KIAA0170 gene product (KIAA0170), mRNA /cds=(14,6283) /gb=NM_014641 /gi=7661965 /ug=Hs.433653 /len=6940	NM_014641	Hs.433653	NP_055456
6592	0.00767	methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,1111) /gb=NM_006636 /gi=13699869 /ug=Hs.154672 /len=2154	NM_006636	Hs.154672	NP_006627
6593	0.019933	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae) (NHP2L1), mRNA /cds=(95,481) /gb=NM_005008 /gi=4826859 /ug=Hs.182255 /len=1475	NM_005008	Hs.182255	NP_004999
6600	0.043451	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone) (GNRH1), mRNA /cds=(1075,1353) /gb=NM_000825 /gi=19923125 /ug=Hs.82963 /len=1512	NM_000825	Hs.82963	NP_000816

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6603	0.001133	tm68a09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2163256 3', mRNA sequence /clone=IMAGE:2163256 /clone_end=3' /gb=AI498805 /gi=4390787 /ug=Hs.436349 /len=460	AI498805	Hs.436349	
6612	0.037084	high-mobility group box 1 (HMGB1), mRNA /cds=(77,724) /gb=NM_002128 /gi=20149538 /ug=Hs.6727 /len=1207	NM_002128	Hs.6727	NP_002119
6618	0.022422	eukaryotic translation elongation factor 1 gamma (EEF1G), mRNA /cds=(38,1351) /gb=NM_001404 /gi=25453475 /ug=Hs.256184 /len=1429	NM_001404	Hs.256184	NP_001395
6623	0.048172	attractin (ATRN), transcript variant 1, mRNA /cds=(80,4369) /gb=NM_139321 /gi=21450860 /ug=Hs.194019 /len=8645	NM_139321	Hs.194019	NP_647538
6630	0.005038	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase) (NDUFS6), mRNA /cds=(11,385) /gb=NM_004553 /gi=4758791 /ug=Hs.49767 /len=547	NM_004553	Hs.49767	NP_004544
6633	0.019933	HSPCO34 protein (LOC51668), mRNA /cds=(58,402) /gb=NM_016126 /gi=7706382 /ug=Hs.46967 /len=598	NM_016126	Hs.46967	NP_057210
6650	0.043451	tetratricopeptide repeat domain 1 (TTC1), mRNA /cds=(51,929) /gb=NM_003314 /gi=4507710 /ug=Hs.7733 /len=1407	NM_003314	Hs.7733	NP_003305
6651	0.028189	tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10), mRNA /cds=(96,941) /gb=NM_003810 /gi=23510439 /ug=Hs.83429 /len=1776	NM_003810	Hs.83429	NP_003801
6654	0.017682	pM5 protein (PM5), mRNA /cds=(1,3669) /gb=NM_014287 /gi=10947030 /ug=Hs.439182 /len=4182	NM_014287	Hs.439182	NP_055102
6666	0.01471	tigger transposable element derived 1 (TIGD1), mRNA /cds=(635,2410) /gb=NM_145702 /gi=22209000 /ug=Hs.351348 /len=2448	NM_145702	Hs.351348	NP_663748
6683	0.021147	lamin A/C (LMNA), transcript variant 1, mRNA /cds=(213,2207) /gb=NM_170707 /gi=27436945 /ug=Hs.377973 /len=3181	NM_170707	Hs.377973	NP_733822
6708	0.043451	erythroid differentiation-related factor 1	AF040247		
6715	0.022422	KIAA0076 gene product (KIAA0076), mRNA /cds=(87,5183) /gb=NM_014780 /gi=7661893 /ug=Hs.51039 /len=5253	NM_014780	Hs.51039	NP_055595
6722	0.025168	syndecan 1 (SDC1), mRNA /cds=(253,1185) /gb=NM_002997 /gi=21359855 /ug=Hs.82109 /len=2484	NM_002997	Hs.82109	NP_002988

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6734	0.031506	PAI-1 mRNA-binding protein (PAI-RBP1), mRNA /cds=(86,1249) /gb=NM_015640 /gi=7661625 /ug=Hs.165998 /len=2201	NM_015640	Hs.165998	NP_056455
6750	0.033283	ADP-ribosylation-like factor 6 interacting protein 4 (ARL6IP4), mRNA /cds=(63,719) /gb=NM_016638 /gi=7706183 /ug=Hs.103561 /len=952	NM_016638	Hs.103561	NP_061164
6752	0.01471	tumor endothelial marker 6 (TEM6), mRNA /cds=(93,3710) /gb=NM_022748 /gi=17511208 /ug=Hs.12210 /len=6702	NM_022748	Hs.12210	NP_073585
6755	0.012975	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 (SLC25A3), nuclear gene encoding mitochondrial protein, transcript variant 1b, mRNA /cds=(49,1134) /gb=NM_002635 /gi=4505774 /ug=Hs.78713 /len=1330	NM_002635	Hs.78713	NP_005879
6760	0.023762	2-hydroxyphytanoyl-CoA lyase (HPCL2), mRNA /cds=(100,1836) /gb=NM_012260 /gi=6912417 /ug=Hs.63290 /len=1976	NM_012260	Hs.63290	NP_036392
6772	0.029809	hypothetical protein FLJ22301 (FLJ22301), mRNA /cds=(696,2054) /gb=NM_024836 /gi=13376246 /ug=Hs.181406 /len=2952	NM_024836	Hs.181406	NP_079112
6794	0.037084	chromosome 13 open reading frame 12 (C13orf12), mRNA /cds=(76,501) /gb=NM_015932 /gi=21361533 /ug=Hs.279813 /len=1352	NM_015932	Hs.279813	NP_057016
6796	0.007162	hypothetical protein, clone 2746033 (HSA272196), mRNA /cds=(39,593) /gb=NM_018405 /gi=24475639 /ug=Hs.8179 /len=861	NM_018405	Hs.8179	NP_060875
6813	0.039115	constitutive photomorphogenic protein (COP1), mRNA /cds=(1,2196) /gb=NM_022457 /gi=21359962 /ug=Hs.105737 /len=2196	NM_022457	Hs.105737	NP_071902
6829	0.023762	transforming growth factor, alpha (TGFA), mRNA /cds=(32,514) /gb=NM_003236 /gi=4507460 /ug=Hs.170009 /len=4119	NM_003236	Hs.170009	NP_003227
6835	0.012975	mRNA for KIAA0191 gene, partial cds. /cds=(1,4553) /gb=D83776 /gi=1228034 /ug=Hs.12413 /len=5203	D83776	Hs.12413	
6846	0.035141	mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant A, mRNA /cds=(306,2045) /gb=NM_003188 /gi=21735560 /ug=Hs.7510 /len=2912	NM_003188	Hs.7510	NP_663306

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6851	0.013819	Similar to expressed sequence AW111961, clone IMAGE:5268751, mRNA /gb=BC041839 /gi=27693117 /ug=Hs.237642 /len=3713	BC041839	Hs.237642	
6861	0.005811	mRNA; cDNA DKFZp434A012 (from clone DKFZp434A012) /gb=AL096752 /gi=5419888 /ug=Hs.306327 /len=2248	AL096752	Hs.306327	
6880	0.031506	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1), nuclear gene encoding mitochondrial protein, mRNA /cds=(463,702) /gb=NM_001864 /gi=18105034 /ug=Hs.421621 /len=783	NM_001864	Hs.421621	NP_001855
6881	0.006684	uncharacterized hematopoietic stem/progenitor cells protein MDS029 (MDS029), mRNA /cds=(112,438) /gb=NM_018464 /gi=8923929 /ug=Hs.43549 /len=636	NM_018464	Hs.43549	NP_060934
6894	0.009383	Werner helicase interacting protein (WHIP), transcript variant 1, mRNA /cds=(192,2189) /gb=NM_020135 /gi=18426901 /ug=Hs.236828 /len=2670	NM_020135	Hs.236828	NP_569079
6920	0.017682	thioredoxin (TXN), mRNA /cds=(64,381) /gb=NM_003329 /gi=4507744 /ug=Hs.432922 /len=501	NM_003329	Hs.432922	NP_003320
6935	0.048172	FtsJ 3 (E. coli) (FTSJ3), mRNA /cds=(72,2615) /gb=NM_017647 /gi=17017990 /ug=Hs.257486 /len=2999	NM_017647	Hs.257486	NP_060117
6941	0.039115	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2 (SMARCC2), transcript variant 1, mRNA /cds=(33,3677) /gb=NM_003075 /gi=21237804 /ug=Hs.236030 /len=4039	NM_003075	Hs.236030	NP_620706
6969	0.010023	oligophrenin 1 (OPHN1), mRNA /cds=(638,3046) /gb=NM_002547 /gi=4505506 /ug=Hs.128824 /len=7350 (=FLJ11206)	NM_002547	Hs.128824	NP_002538
6972	0.035141	similar to zinc finger protein (LOC91172), mRNA (=FLJ12859,=FLJ11645)	XM_036627		
6974	0.045762	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa (NDUFAB1), mRNA /cds=(25,495) /gb=NM_005003 /gi=4826851 /ug=Hs.5556 /len=663	NM_005003	Hs.5556	NP_004994
6989	0.012175	transmembrane 9 superfamily member 1 (TM9SF1), mRNA /cds=(35,1855) /gb=NM_006405 /gi=21361314 /ug=Hs.91586 /len=2138	NM_006405	Hs.91586	NP_006396

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7005	0.005811	clone MGC:24133 IMAGE:4693393, mRNA, complete cds /cds=(61,528) /gb=BC017973 /gi=22450811 /ug=Hs.288010 /len=946	BC017973	Hs.288010	NP_777556
7022	0.019933	ribosomal protein S29 (RPS29), mRNA /cds=(31,201) /gb=NM_001032 /gi=13904868 /ug=Hs.539 /len=346	NM_001032	Hs.539	NP_001023
7033	0.029809	vacuolar protein sorting 35 (yeast) (VPS35), mRNA /cds=(48,2438) /gb=NM_018206 /gi=17999540 /ug=Hs.264190 /len=2707	NM_018206	Hs.264190	NP_060676
7042	0.047799	mRNA for KIAA0261 gene, partial cds. /cds=(1,3866) /gb=D87450 /gi=1665788 /ug=Hs.154978 /len=6155	D87450	Hs.154978	
7043	0.009383	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), mRNA /cds=(556,1788) /gb=NM_000430 /gi=6031206 /ug=Hs.77318 /len=5581	NM_000430	Hs.77318	NP_000421
7048	0.012975	twisted gastrulation 1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=NM_020648 /gi=21314788 /ug=Hs.247302 /len=3693	NM_020648	Hs.247302	NP_065699
7068	3.16E-04	KIAA1128 protein (KIAA1128), mRNA /cds=(553,2253) /gb=NM_018999 /gi=24308130 /ug=Hs.81897 /len=7248	NM_018999	Hs.81897	NP_061872
7097	0.037084	translocating chain-associating membrane protein (TRAM), mRNA /cds=(92,1216) /gb=NM_014294 /gi=19923404 /ug=Hs.4147 /len=2722	NM_014294	Hs.4147	NP_055109
7098	0.039115	inactive progesterone receptor, 23 kD (TEBP), mRNA /cds=(107,589) /gb=NM_006601 /gi=23308578 /ug=Hs.278270 /len=1490	NM_006601	Hs.278270	NP_006592
7102	0.010023	survival of motor neuron protein interacting protein 1 (SIP1), mRNA /cds=(84,926) /gb=NM_003616 /gi=4506960 /ug=Hs.102456 /len=1285	NM_003616	Hs.102456	NP_003607
7107	0.00767	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function) (ENPP4), mRNA /cds=(49,1410) /gb=NM_014936 /gi=7662357 /ug=Hs.54037 /len=4312	NM_014936	Hs.54037	NP_055751
7127	0.026643	actin-related protein 10 (S. cerevisiae) (ACTR10), mRNA /cds=(81,1334) /gb=NM_018477 /gi=8923711 /ug=Hs.274369 /len=1621	NM_018477	Hs.274369	NP_060947

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7143	0.041237	benzodiazapine receptor (peripheral) (BZRP), nuclear gene encoding mitochondrial protein, transcript variant PBR, mRNA /cds=(88,597) /gb=NM_000714 /gi=21536444 /ug=Hs.202 /len=848	NM_000714	Hs.202	NP_009295
7166	0.01471	transducer of ERBB2, 1 (TOB1), mRNA /cds=(36,1073) /gb=NM_005749 /gi=22035666 /ug=Hs.178137 /len=1830	NM_005749	Hs.178137	NP_005740
7175	0.029809	AGENCOURT_6853421 NIH_MGC_99 cDNA clone IMAGE:5926418 5', mRNA sequence /clone=IMAGE:5926418 /clone_end=5' /gb=BQ064669 /gi=19893520 /ug=Hs.380699 /len=969	BQ064669	Hs.380699	
7176	0.012175	tumor protein, translationally-controlled 1 (TPT1), mRNA /cds=(95,613) /gb=NM_003295 /gi=4507668 /ug=Hs.401448 /len=830	NM_003295	Hs.401448	NP_003286
7178	0.005412	supervillin (SVIL), transcript variant 2, mRNA /cds=(754,7398) /gb=NM_021738 /gi=11496981 /ug=Hs.154567 /len=8300	NM_021738	Hs.154567	NP_068506
7187	0.015649	collagen, type V, alpha 1 (COL5A1), mRNA /cds=(383,5899) /gb=NM_000093 /gi=16554578 /ug=Hs.146428 /len=6496	NM_000093	Hs.146428	NP_000084
7201	0.043451	glutathione peroxidase 1 (GPX1), mRNA /cds=(319,924) /gb=NM_000581 /gi=10834975 /ug=Hs.76686 /len=1134	NM_000581	Hs.76686	NP_000572
7234	0.00104	chemokine-like factor 1 (CKLF1), mRNA /cds=(148,606) /gb=NM_016951 /gi=10092593 /ug=Hs.15159 /len=689	NM_016951	Hs.15159	NP_058647
7240	0.023762	block of proliferation 1 (BOP1), mRNA /cds=(43,2283) /gb=NM_015201 /gi=21389316 /ug=Hs.30736 /len=2396	NM_015201	Hs.30736	NP_056016
7243	6.11E-04	calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2), transcript variant 1, mRNA /cds=(830,2596) /gb=NM_006549 /gi=27437014 /ug=Hs.108708 /len=5620	NM_006549	Hs.108708	NP_757380
7244	0.011417	Nedd-4-like ubiquitin-protein ligase, clone MGC:17353 IMAGE:3453212, mRNA, complete cds	BC013645.1	Hs.333382	AAH13645.1
7279	0.028189	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1), mRNA /cds=(205,6969) /gb=NM_018429 /gi=21281668 /ug=Hs.272808 /len=7207	NM_018429	Hs.272808	NP_060899

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7283	0.048172	HSPC056 protein (HSPC056), mRNA /cds=(145,972) /gb=NM_014154 /gi=7661763 /ug=Hs.422287 /len=2879	NM_014154	Hs.422287	NP_054873
7284	0.033283	GK003 protein (GK003), mRNA /cds=(10,690) /gb=NM_020192 /gi=21281666 /ug=Hs.83313 /len=901	NM_020192	Hs.83313	NP_064577
7285	0.043451	MR4-ET0140-070501-014-g01 ET0140 cDNA, mRNA sequence /gb=BQ331564 /gi=20972721 /ug=Hs.442329 /len=219	BQ331564	Hs.442329	
7288	0.022422	KIAA0800 gene product (KIAA0800), mRNA /cds=(169,4692) /gb=NM_014703 /gi=7662315 /ug=Hs.118738 /len=5984	NM_014703	Hs.118738	NP_055518
7310	0.023762	UI-H-BI2-agp-f-12-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2725031 3', mRNA sequence /clone=IMAGE:2725031 /clone_end=3' /gb=AW292456 /gi=6699092 /ug=Hs.437793 /len=745	AW292456	Hs.437793	
7313	0.048172	translocation protein 1 (TLOC1), mRNA /cds=(613,1812) /gb=NM_003262 /gi=14602425 /ug=Hs.8146 /len=3091	NM_003262	Hs.8146	NP_003253
7319	0.039115	mRNA for KIAA0276 gene, partial cds. /cds=(1,932) /gb=D87466 /gi=1665816 /ug=Hs.240112 /len=4185	D87466	Hs.240112	
7320	0.006684	RNA-binding region (RNP1, RRM) containing 4 (RNPC4), mRNA /cds=(187,1461) /gb=NM_018107 /gi=21361701 /ug=Hs.4997 /len=2442	NM_018107	Hs.4997	NP_060577
7321	0.017682	translocase of inner mitochondrial membrane 17 A (yeast) (TIMM17A), mRNA /cds=(8,523) /gb=NM_006335 /gi=5454119 /ug=Hs.20716 /len=1645	NM_006335	Hs.20716	NP_006326
7322	0.031506	BM-017 (=ALEX3)	AF208859		NP_808817
7331	0.037084	AGENCOURT_8856629 Lupski_sciatic_nerve cDNA clone IMAGE:6200636 5', mRNA sequence /clone=IMAGE:6200636 /clone_end=5' /gb=BQ947179 /gi=22362657 /ug=Hs.356605 /len=1277	BQ947179	Hs.356605	
7343	0.007162	hypothetical protein FLJ12619 (FLJ12619), mRNA /cds=(539,1228) /gb=NM_030939 /gi=21359961 /ug=Hs.7779 /len=2444	NM_030939	Hs.7779	NP_112201
7349	0.005412	dermatopontin (DPT), mRNA /cds=(7,612) /gb=NM_001937 /gi=4755134 /ug=Hs.80552 /len=717	NM_001937	Hs.80552	NP_001928

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7357	0.008208	chromosome 6 open reading frame 33 (C6orf33), mRNA /cds=(165,1229) /gb=NM_133367 /gi=19115959 /ug=Hs.239388 /len=4650	NM_133367	Hs.239388	NP_588608
7360	0.028189	clone IMAGE:5016712, mRNA /gb=BC032119 /gi=22749564 /ug=Hs.400876 /len=1185	BC032119	Hs.400876	
7361	0.037084	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 (SMARCA4), mRNA /cds=(277,5220) /gb=NM_003072 /gi=21071055 /ug=Hs.78202 /len=5681	NM_003072	Hs.78202	NP_003063
7378	0.022422	regulator of G-protein signalling 10 (RGS10), mRNA /cds=(44,547) /gb=NM_002925 /gi=11184225 /ug=Hs.82280 /len=664	NM_002925	Hs.82280	NP_002916
7387	0.037157	ribosomal protein L4 (RPL4), mRNA /cds=(57,1340) /gb=NM_000968 /gi=16579884 /ug=Hs.286 /len=1449	NM_000968	Hs.286	NP_000959
7390	0.045762	peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA /cds=(45,542) /gb=NM_021130 /gi=10863926 /ug=Hs.401787 /len=753	NM_021130	Hs.401787	NP_066953
7414	6.69E-04	tetraspanin similar to TM4SF9 (DC-TM4F2), mRNA /cds=(79,891) /gb=NM_030927 /gi=13569888 /ug=Hs.101395 /len=2556	NM_030927	Hs.101395	NP_112189
7420	0.029809	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) (GALNT1), mRNA /cds=(32,1711) /gb=NM_020474 /gi=13124890 /ug=Hs.80120 /len=3778	NM_020474	Hs.80120	NP_065207
7427	0.003487	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_153649	Hs.85844	NP_705935
7455	0.039115	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) (AGPAT2), mRNA /cds=(67,903) /gb=NM_006412 /gi=6041664 /ug=Hs.209119 /len=1522	NM_006412	Hs.209119	NP_006403
7491	0.019933	chromosome 20 open reading frame 149 (C20orf149), mRNA /cds=(150,494) /gb=NM_024299 /gi=13236523 /ug=Hs.79625 /len=803	NM_024299	Hs.79625	NP_077275
7508	0.012175	mRNA for RCC1-like protein (TD-60 gene) /cds=(236,1804) /gb=AJ421269 /gi=27526612 /ug=Hs.284146 /len=4114	AJ421269	Hs.284146	NP_061185

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7548	0.015649	methionine adenosyltransferase II, beta (MAT2B), mRNA /cds=(73,1077) /gb=NM_013283 /gi=20127525 /ug=Hs.54642 /len=2054	NM_013283	Hs.54642	NP_037415
7574	0.039115	ubiquitin-conjugating enzyme E2N (UBC13 yeast) (UBE2N), mRNA /cds=(64,522) /gb=NM_003348 /gi=4507792 /ug=Hs.75355 /len=1203	NM_003348	Hs.75355	NP_003339
7576	0.002192	cytochrome P450, family 1, subfamily B, polypeptide 1 (CYP1B1), mRNA /cds=(373,2004) /gb=NM_000104 /gi=13325059 /ug=Hs.154654 /len=5128	NM_000104	Hs.154654	NP_000095
7577	0.00767	chromosome 14 open reading frame 108 (C14orf108), mRNA /cds=(407,1879) /gb=NM_018229 /gi=21361775 /ug=Hs.106210 /len=3088	NM_018229	Hs.106210	NP_060699
7581	0.017682	FK506 binding protein 5 (FKBP5), mRNA /cds=(154,1527) /gb=NM_004117 /gi=17149847 /ug=Hs.7557 /len=3781	NM_004117	Hs.7557	NP_004108
7587	3.83E-04	XPA binding protein 1; putative ATP(GTP)-binding protein (NTPBP), mRNA /cds=(25,1149) /gb=NM_007266 /gi=14149628 /ug=Hs.18259 /len=1829	NM_007266	Hs.18259	NP_009197
7599	0.012975	fibrinogen, B beta polypeptide (FGB), mRNA /cds=(9,1484) /gb=NM_005141 /gi=11761630 /ug=Hs.7645 /len=1918	NM_005141	Hs.7645	NP_005132
7600	0.033283	hypothetical protein MGC45400 (MGC45400), mRNA /cds=(245,598) /gb=NM_153333 /gi=23503246 /ug=Hs.389734 /len=1290	NM_153333	Hs.389734	NP_699164
7618	0.037084	hypothetical protein FLJ11240 (FLJ11240), mRNA /cds=(26,1648) /gb=NM_018368 /gi=8922955 /ug=Hs.339833 /len=1947	NM_018368	Hs.339833	NP_060838
7623	0.009969	growth factor receptor-bound protein 10 (GRB10), mRNA /cds=(782,2548) /gb=NM_005311 /gi=19923302 /ug=Hs.81875 /len=5431	NM_005311	Hs.81875	NP_005302
7637	0.012975	serum response factor (c-fos serum response element-binding transcription factor) (SRF), mRNA /cds=(359,1885) /gb=NM_003131 /gi=4507204 /ug=Hs.155321 /len=4201	NM_003131	Hs.155321	NP_003122
7642	0.048172	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
7694	4.70E-05	cDNA FLJ25013 fis, clone CBL01365. /gb=AK057742 /gi=16553667 /ug=Hs.380091 /len=2200	AK057742	Hs.380091	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7697	0.045762	thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=NM_006472 /gi=5454161 /ug=Hs.179526 /len=2704	NM_006472	Hs.179526	NP_006463
7724	0.003233	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), mRNA /cds=(252,1457) /gb=NM_002546 /gi=22547122 /ug=Hs.81791 /len=2291	NM_002546	Hs.81791	NP_002537
7730	0.001342	MTB (MTB) mRNA, complete cds /cds=(80,265) /gb=AF348994 /gi=28190031 /ug=Hs.333727 /len=408	AF348994	Hs.333727	NP_783321
7731	0.005412	cDNA FLJ14844 fis, clone PLACE1000133, highly similar to TRANSCRIPTION FACTOR BTF3. /cds=(91,567) /gb=AK027750 /gi=14042660 /ug=Hs.93748 /len=2203	AK027750	Hs.93748	
7753	0.017682	SAC1 suppressor of actin mutations 1-like (yeast) (SACM1L), mRNA /cds=(70,1833) /gb=NM_014016 /gi=7662337 /ug=Hs.5867 /len=3572	NM_014016	Hs.5867	NP_054735
7807	0.011417	poly(A) polymerase gamma (PAPOLG), mRNA /cds=(232,2442) /gb=NM_022894 /gi=16306567 /ug=Hs.146123 /len=4252	NM_022894	Hs.146123	NP_075045
7839	0.023762	EST(xc43h04.x1 NCI_CGAP_Co20 clone IMAGE:2587063 3' gb:M99436 TRANSDUCIN-LIKE ENHANCER PROTEIN 2)	AW081723		NP_003251
7873	0.002024	BX098638 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998G14405, mRNA sequence /clone=IMAGp998G14405_/_IMAGE:208165 /gb=BX098638 /gi=27829530 /ug=Hs.435496 /len=438	BX098638	Hs.435496	
7908	0.031506	EST EST43399 Fetal brain I cDNA 3' end	AA338448		NP_112577
7941	0.00767	EST (EST370348 MAGE resequences, MAGE cDNA)	AW958278		NP_112420
7951	0.008208	EST (am59f03.x1 Johnston frontal	AI124626		
7968	0.031506	low density lipoprotein receptor-related protein 5 (LRP5), mRNA /cds=(49,4896) /gb=NM_002335 /gi=4505018 /ug=Hs.6347 /len=5100	NM_002335	Hs.6347	NP_002326
7985	0.035141	SH3-domain GRB2-like 3 (SH3GL3), mRNA /cds=(493,1560) /gb=NM_003027 /gi=20070145 /ug=Hs.80315 /len=2015	NM_003027	Hs.80315	NP_003018

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7991	0.033283	hypothetical protein FLJ20425 (LYAR), mRNA /cds=(189,1328) /gb=NM_017816 /gi=8923397 /ug=Hs.425427 /len=1598	NM_017816	Hs.425427	NP_060286
8020	0.023762	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART), mRNA /cds=(79,3111) /gb=NM_000819 /gi=24475881 /ug=Hs.82285 /len=3291	NM_000819	Hs.82285	NP_780294
8054	0.011417	pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence /cds=UNKNOWN/gb=AF334710 /gi=12658438 /ug=Hs.8364 /len=1819	AF334710	Hs.8364	NP_002603
8056	0.00767	ADP-ribosyltransferase (NAD ; poly (ADP-ribose) polymerase) (ADPRT), mRNA /cds=(160,3204) /gb=NM_001618 /gi=11496989 /ug=Hs.177766 /len=3859	NM_001618	Hs.177766	NP_001609
8076	0.041237	hypothetical protein PRO2577 (PRO2577), mRNA /cds=(492,665) /gb=NM_018630 /gi=8924181 /ug=Hs.241576 /len=1032	NM_018630	Hs.241576	
8097	0.027996	mRNA for KIAA1915 protein, partial cds. /cds=(356,2536) /gb=AB067502 /gi=15620888 /ug=Hs.12915 /len=7801	AB067502	Hs.12915	
8191	0.035141	downstream neighbor of SON (DONSON), transcript variant 1, mRNA /cds=(68,1768) /gb=NM_017613 /gi=22035582 /ug=Hs.17834 /len=2189	NM_017613	Hs.17834	NP_665738
8198	0.039115	PHD zinc finger protein XAP135 (XAP135), transcript variant 2, mRNA /cds=(222,1448) /gb=NM_133325 /gi=19747275 /ug=Hs.7759 /len=1583	NM_133325	Hs.7759	NP_579866
8203	0.019933	hypothetical protein FLJ14668 (FLJ14668), mRNA /cds=(59,475) /gb=NM_032822 /gi=14249519 /ug=Hs.334644 /len=1786	NM_032822	Hs.334644	NP_116211
8230	0.01471	mRNA for KIAA0592 protein, partial cds. /cds=(1,4062) /gb=AB011164 /gi=3043707 /ug=Hs.439367 /len=4623	AB011164	Hs.439367	
8272	0.043451	EST(PM4-BT0650-010400-002-a06 BT0650)	BE083882		NP_060487
8308	0.004048	EST(ty24e09.x1 NCI_CGAP_Ut3 clone IMAGE:2280040 3' contains Alu repeat)	AI758800		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8309	0.002773	hypothetical protein FLJ14906 (FLJ14906), mRNA /cds=(131,736) /gb=NM_032859 /gi=14249591 /ug=Hs.183528 /len=2492	NM_032859	Hs.183528	NP_116248
8333	0.035141	EST (fb12g02.x1 zebrafish fin day0 regeneration)	AI384158		
8341	0.019933	EST(we27d09.x1 NCI_CGAP_Lu24 clone IMAGE:2342321 3')	AI797144		NP_002877
8359	0.035141	UI-H-BW1-amn-b-05-0-UI.s1 NCI_CGAP_Sub7 cDNA clone IMAGE:3070401 3', mRNA sequence /clone=IMAGE:3070401 /clone_end=3' /gb=BF513064 /gi=11598243 /ug=Hs.446233 /len=777	BF513064	Hs.446233	
8373	0.035141	NISC_gj17d11.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:3272108 3', mRNA sequence /clone=IMAGE:3272108 /clone_end=3' /gb=CB050438 /gi=27788725 /ug=Hs.435309 /len=534	CB050438	Hs.435309	
8381	0.010023	Tho2 mRNA, complete cds /cds=(1,4437) /gb=AF441770 /gi=20799317 /ug=Hs.16411 /len=4452	AF441770	Hs.16411	
8411	0.017682	UI-1-BB1p-aya-d-12-0-UI.s1 NCI_CGAP_PI6 cDNA clone UI-1-BB1p-aya-d-12-0-UI 3', mRNA sequence /clone=UI-1-BB1p-aya-d-12-0-UI /clone_end=3' /gb=BU754499 /gi=23713459 /ug=Hs.432873 /len=1196	BU754499	Hs.432873	
8435	0.019933	BX099435 NCI_CGAP_Co8 cDNA clone IMAGp998M083951, mRNA sequence /clone=IMAGp998M083951; IMAGE:1559599 /gb=BX099435 /gi=27829993 /ug=Hs.126589 /len=659	BX099435	Hs.126589	
8438	0.017682	mRNA sequence /gb=L26969 /gi=16905391 /ug=Hs.362852 /len=1738	L26969	Hs.362852	
8459	0.003487	zs54b10.r1 NCI_CGAP_GCB1 cDNA clone IMAGE:701275 5', mRNA sequence /clone=IMAGE:701275 /clone_end=5' /gb=AA287780 /gi=1933461 /ug=Hs.369808 /len=497	AA287780	Hs.369808	
8472	0.037084	cDNA FLJ14188 fis, clone NT2RP2005980. /gb=AK024250 /gi=10436579 /ug=Hs.288671 /len=2289	AK024250	Hs.288671	
8480	0.031506	ribosomal protein L37a (RPL37A), mRNA /cds=(36,314) /gb=NM_000998 /gi=16306561 /ug=Hs.296290 /len=392	NM_000998	Hs.296290	NP_000989
8486	0.043451	cDNA, 3' end /clone=IMAGE:1935382 /clone_end=3' /gb=AI340092 /gi=4077019 /ug=Hs.327321 /len=361	AI340092	Hs.327321	NP_002370

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8492	0.003233	EST CM2-BT0857-021100-470-g06 BT0857 Homo sapiens cDNA	BF745663		
8514	0.041237	mRNA; cDNA DKFZp451B1818 (from clone DKFZp451B1818) /gb=AL832623 /gi=21733198 /ug=Hs.77554 /len=6240	AL832623	Hs.77554	
8516	0.039115	EST (MR1-SN0033-100400-001-a10 SN0033)	AW867013		
8529	0.004357	EST (602645742F1 NIH_MGC_76 clone IMAGE:4767299 5')	BG618375		
8530	0.045762	UI-E-EJ0-ahq-g-22-0-UI.s1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahq-g-22-0-UI 3', mRNA sequence /clone=UI-E-EJ0-ahq-g-22-0-UI /clone_end=3' /gb=BM674631 /gi=18984529 /ug=Hs.444500 /len=1272	BM674631	Hs.444500	
8546	0.045762	EST(hc98c08.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2908046 3' similar to TR:O14792 O14792 HEPARAN SULFATE 3-O-SULFOTRANSFERASE-1 PRECURSOR)	AW340546		NP_005105
8547	0.019933	cDNA FLJ36837 fis, clone ASTRO2011422. /gb=AK094156 /gi=21753158 /ug=Hs.36475 /len=3302	AK094156	Hs.36475	
8557	0.018779	UI-H-ED0-awy-a-01-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5825160 3', mRNA sequence /clone=IMAGE:5825160 /clone_end=3' /gb=BQ017647 /gi=19752924 /ug=Hs.124747 /len=1445	BQ017647	Hs.124747	
8560	0.012175	ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500	NM_000991	Hs.356371	NP_000982
8564	0.039115	EST(cDNA clone IMAGE:2569171 3')	AW073383		
8595	0.017682	ribosomal protein L3 (RPL3), mRNA /cds=(27,1238) /gb=NM_000967 /gi=16507968 /ug=Hs.119598 /len=1311	NM_000967	Hs.119598	NP_000958
8606	0.011736	hypothetical protein DKFZp451G182 (DKFZp451G182), mRNA /cds=(99,4049) /gb=NM_153610 /gi=23957703 /ug=Hs.50794 /len=4678	NM_153610	Hs.50794	NP_705838
8646	0.001585	cDNA FLJ39413 fis, clone PLACE6015729. /gb=AK096732 /gi=21756291 /ug=Hs.194339 /len=1957	AK096732	Hs.194339	
8669	0.005412	cDNA FLJ10190 fis, clone HEMBA1004753. /gb=AK001052 /gi=7022081 /ug=Hs.274546 /len=1318	AK001052	Hs.274546	
8673	0.012175	jun1.P1.D7 conorm cDNA 3', mRNA sequence /clone_end=3' /gb=AI535800 /gi=4449935 /ug=Hs.369112 /len=480	AI535800	Hs.369112	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8675	0.002372	UI-H-EI0-ayo-a-20-0-UI.s1 NCI_CGAP_EI0 cDNA clone IMAGE:5841307 3', mRNA sequence /clone=IMAGE:5841307 /clone_end=3' /gb=BQ004581 /gi=19729481 /ug=Hs.412459 /len=1095	BQ004581	Hs.412459	
8738	0.041237	tb26b01.x1 NCI_CGAP_Kid12 cDNA clone IMAGE:2055433 3' similar to contains Alu repetitive element;, mRNA sequence /clone=IMAGE:2055433 /clone_end=3' /gb=AI308217 /gi=4002852 /ug=Hs.177064 /len=421	AI308217	Hs.177064	
8746	0.018779	tg02e02.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2107610 3', mRNA sequence /clone=IMAGE:2107610 /clone_end=3' /gb=AI380429 /gi=4190282 /ug=Hs.172445 /len=478	AI380429	Hs.172445	
8769	0.033283	EST(adult brain Danio rerio cDNA clone 4966301 5' similar to SW:RLA1_CHICK P18660 60S ACIDIC RIBOSOMAL PROTEIN P1. ;contains element MER22 repetitive element ;)	BI429083		
8771	0.035141	mitochondrion, complete genome	NC_001807		
8781	0.011417	cDNA: FLJ20933 fis, clone ADSE01388. /gb=AK024586 /gi=10436898 /ug=Hs.296757 /len=1567	AK024586	Hs.296757	
8788	0.012975	ESTs, cDNA /gb=AW978555 /gi=8169822 /ug=Hs.92448 /len=754	AW978555	Hs.92448	
8828	0.037084	cDNA FLJ13443 fis, clone PLACE1002853	AK023505		NP_078968
8837	0.003487	no significant match	SEQ.ID.No.39		
8838	0.048172	No significant match	SEQ.ID.No.45		
8840	0.019933	No significant match	SEQ.ID.No.54		
8856	0.003233	control			
8874	0.026411	No significant match (ORF:+1:256~491[237])	SEQ.ID.No.26		
8946	0.018779	hypothetical protein FLJ33282 (FLJ33282), mRNA /cds=(225,1523) /gb=NM_152388 /gi=22748830 /ug=Hs.346509 /len=2078	NM_152388	Hs.346509	
8949	0.029809	tx18g05.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2269592 3', mRNA sequence /clone=IMAGE:2269592 /clone_end=3' /gb=AI612954 /gi=4622121 /ug=Hs.187303 /len=205	AI612954	Hs.187303	
8967	0.032562	hypothetical protein FLJ13231 (FLJ13231), mRNA /cds=(134,1255) /gb=NM_023073 /gi=12751482 /ug=Hs.156148 /len=2642	NM_023073	Hs.156148	NP_075561

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8972	0.023762	EST (ym20a08.r1 Soares infant brain 1NIB IMAGE:48353 5')	H15948		
8981	0.006234	AV737351 CB cDNA clone CBLALE11 5', mRNA sequence /clone=CBLALE11 /clone_end=5' /gb=AV737351 /gi=10854932 /ug=Hs.444989 /len=511	AV737351	Hs.444989	
8988	0.019933	hypothetical protein FLJ36674 (FLJ36674), mRNA /cds=(26,484) /gb=NM_173622 /gi=27734737 /ug=Hs.164595 /len=2236	NM_173622	Hs.164595	NP_775893
8990	0.028189	hypothetical protein FLJ39514 (FLJ39514), mRNA /cds=(121,2040) /gb=NM_152540 /gi=22749126 /ug=Hs.48565 /len=2221	NM_152540	Hs.48565	NP_689753
9061	0.037084	cDNA FLJ33960 fis, clone CTONG2018843. /gb=AK091279 /gi=21749612 /ug=Hs.126465 /len=2849	AK091279	Hs.126465	
9072	0.035141	clone MGC:20469 IMAGE:4554554, mRNA, complete cds /cds=(208,1149) /gb=BC012182 /gi=15082546 /ug=Hs.82508 /len=1862	BC012182	Hs.82508	
9096	0.041237	C1q and tumor necrosis factor related protein 7 (C1QTNF7), mRNA /cds=(234,1103) /gb=NM_031911 /gi=21314748 /ug=Hs.153714 /len=3959	NM_031911	Hs.153714	NP_114117
9106	0.023762	yz39f06.s1 Morton Fetal Cochlea cDNA clone IMAGE:285443 3', mRNA sequence /clone=IMAGE:285443 /clone_end=3' /gb=N66393 /gi=1218518 /ug=Hs.102754 /len=618	N66393	Hs.102754	
9108	3.48E-04	UI-H-EI0-aye-c-17-0-UI.s1 NCI_CGAP_EI0 cDNA clone UI-H-EI0-aye-c-17-0-UI 3', mRNA sequence /clone=UI-H-EI0-aye-c-17-0-UI /clone_end=3' /gb=CA447385 /gi=24811805 /ug=Hs.420740 /len=812	CA447385	Hs.420740	
9174	0.012975	UI-E-EJ0-ahs-e-16-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahs-e-16-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahs-e-16-0-UI /clone_end=5' /gb=BM714718 /gi=19027976 /ug=Hs.446458 /len=1136	BM714718	Hs.446458	
9244	0.021147	Mus musculus mitochondrion, complete genome	NC_001569		
9266	0.018779	clone FLB2932 mRNA sequence /gb=AF138859 /gi=7340965 /ug=Hs.274405 /len=2990	AF138859	Hs.274405	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9274	0.001585	mRNA; cDNA DKFZp586G2120 (from clone DKFZp586G2120); complete cds /cds=(19,2604) /gb=AL136924/gi=12053342 /ug=Hs.62349 /len=4137	AL136924	Hs.62349	NP_061866
9275	0.003758	ESTs, cDNA, 5' end /clone=IMAGE:3857750 /clone_end=5' /gb=BF035134 /gi=10742846 /ug=Hs.195789 /len=847	BF035134	Hs.195789	
9310	0.001585	No significant match	SEQ.ID.No.71		
9311	0.018779	Novel, ORF+1(73~201)	SEQ.ID.No.75		
9315	0.037084	No significant match	SEQ.ID.No.89		
9372	0.012175	chromosome 17 open reading frame 35 (C17orf35), mRNA /cds=(259,837) /gb=NM_003876 /gi=4505900 /ug=Hs.15196 /len=1211	NM_003876	Hs.15196	NP_003867
9399	0.002773	NPD002 protein (NPD002), mRNA /cds=(89,1954) /gb=NM_014049 /gi=21361496 /ug=Hs.7010 /len=2494	NM_014049	Hs.7010	NP_054768
9407	0.011417	adenylate kinase 3 like 1 (AK3L1), mRNA /cds=(141,824) /gb=NM_016282 /gi=19923436 /ug=Hs.43436 /len=2642	NM_016282	Hs.43436	NP_057366
9417	0.00767	Siah-interacting protein (SIP), mRNA /cds=(118,804) /gb=NM_014412 /gi=7656951 /ug=Hs.27258 /len=2435	NM_014412	Hs.27258	NP_055227
9457	0.022422	serine/threonine kinase 17a (apoptosis-inducing) (STK17A), mRNA /cds=(118,1362) /gb=NM_004760 /gi=4758191 /ug=Hs.9075 /len=2641	NM_004760	Hs.9075	NP_004751
9459	0.010023	ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA /cds=(54,389) /gb=NM_006294 /gi=20070231 /ug=Hs.131255 /len=965	NM_006294	Hs.131255	NP_006285
9473	0.011417	mRNA; cDNA DKFZp564D152 (from clone DKFZp564D152); complete cds /cds=(99,1415) /gb=AL136629 /gi=12052783 /ug=Hs.278479 /len=3229	AL136629	Hs.278479	
9485	0.012975	mRNA; cDNA DKFZp434K1412 (from clone DKFZp434K1412) /gb=AL137753 /gi=6808455 /ug=Hs.12144 /len=5448	AL137753	Hs.12144	
9486	0.048172	neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), mRNA /cds=(259,1344) /gb=NM_004404 /gi=4758157 /ug=Hs.155595 /len=3433	NM_004404	Hs.155595	NP_004395
9489	0.015649	similar to putative (H. sapiens) (LOC129641), mRNA	XM_059369		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9492	0.048653	601846634F1 NIH_MGC_55 cDNA clone IMAGE:4077632 5', mRNA sequence /clone=IMAGE:4077632 /clone_end=5' /gb=BF214729 /gi=11108315 /ug=Hs.446581 /len=835	BF214729	Hs.446581	
9498	0.048172	PFTAIRE protein kinase 1 (PFTK1), mRNA /cds=(145,1500) /gb=NM_012395 /gi=6912583 /ug=Hs.57856 /len=4957	NM_012395	Hs.57856	NP_036527
9511	0.028189	emopamil binding related protein, delta8-delta7 sterol isomerase related protein (EBRP), mRNA /cds=(53,673) /gb=NM_032565 /gi=14211872 /ug=Hs.433278 /len=931	NM_032565	Hs.433278	NP_115954
9513	0.035141	hypothetical gene supported by AY007122 (LOC92719), mRNA	XM_046853		
9530	0.004048	hypothetical protein FLJ10856 (FLJ10856), mRNA /cds=(148,1233) /gb=NM_018247 /gi=8922719 /ug=Hs.108530 /len=3720	NM_018247	Hs.108530	NP_060717
9547	0.048172	mitochondrion, complete genome	NC_001807		
9548	0.033283	ubiquitin specific protease 1 (USP1), mRNA /cds=(246,2603) /gb=NM_003368 /gi=21361109 /ug=Hs.35086 /len=3379	NM_003368	Hs.35086	NP_003359
9561	0.037084	phosphatidylinositol transfer protein, beta (PITPNB), mRNA /cds=(40,855) /gb=NM_012399 /gi=19923401 /ug=Hs.7370 /len=2906	NM_012399	Hs.7370	NP_036531
9595	0.001459	hypothetical protein MGC4701 (MGC4701), mRNA /cds=(149,1585) /gb=NM_024511 /gi=24308290 /ug=Hs.421054 /len=1686	NM_024511	Hs.421054	NP_078787
9596	0.001867	vimentin (VIM), mRNA /cds=(123,1523) /gb=NM_003380 /gi=4507894 /ug=Hs.297753 /len=1851	NM_003380	Hs.297753	NP_000995
9610	0.017682	nuclear DNA-binding protein (C1D), transcript variant 1, mRNA /cds=(64,489) /gb=NM_006333 /gi=27894371 /ug=Hs.15164 /len=1200	NM_006333	Hs.15164	NP_775269
9648	0.025168	Similar to RIKEN cDNA 1500009M05 gene, clone MGC:40370 IMAGE:5105935, mRNA, complete cds /cds=(45,452) /gb=BC032300 /gi=21619026 /ug=Hs.295953 /len=1617	BC032300	Hs.295953	
9712	0.026643	w154c05.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2428712 3', mRNA sequence /clone=IMAGE:2428712 /clone_end=3' /gb=AI864553 /gi=5528660 /ug=Hs.371597 /len=474	AI864553	Hs.371597	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9721	0.045762	EST(yj01e06.r1 clone 147490 5')	R81297		NP_057707
9730	0.035141	601862578F1 NIH_MGC_53 cDNA clone IMAGE:4082082 5', mRNA sequence /clone=IMAGE:4082082 /clone_end=5' /gb=BF207870 /gi=11101456 /ug=Hs.396179 /len=756	BF207870	Hs.396179	
9769	0.043451	AGENCOURT_6445786 NIH_MGC_92 cDNA clone IMAGE:5587250 5', mRNA sequence /clone=IMAGE:5587250 /clone_end=5' /gb=BM468951 /gi=18517993 /ug=Hs.275340 /len=967	BM468951	Hs.275340	
9774	0.031506	cDNA FLJ36605 fis, clone TRACH2015316, highly similar to VIMENTIN. /cds=(631,1317) /gb=AK093924 /gi=21752883 /ug=Hs.379100 /len=2665	AK093924	Hs.379100	
9833	0.004687	AGENCOURT_6861057 NIH_MGC_99 cDNA clone IMAGE:5931113 5', mRNA sequence /clone=IMAGE:5931113 /clone_end=5' /gb=BQ066467 /gi=19895513 /ug=Hs.446485 /len=1029	BQ066467	Hs.446485	
9886	0.005811	mRNA; cDNA DKFZp451F1910 (from clone DKFZp451F1910) /gb=AL833265 /gi=21733898 /ug=Hs.332030 /len=5254	AL833265	Hs.332030	
9921	0.033283	hypothetical protein FLJ10477 (FLJ10477), mRNA /cds=(232,873) /gb=NM_018105 /gi=8922445 /ug=Hs.7432 /len=2167	NM_018105	Hs.7432	NP_060575
9965	0.039115	hypothetical protein DKFZp434K1421 (DKFZP434K1421), mRNA /cds=(29,1705) /gb=NM_032141 /gi=14149806 /ug=Hs.374609 /len=2547	NM_032141	Hs.374609	NP_115517
9972	0.035141	caldesmon 1 (CALD1), transcript variant 1, mRNA /cds=(230,2611) /gb=NM_033138 /gi=15149460 /ug=Hs.325474 /len=3610	NM_033138	Hs.325474	NP_149347
10011	0.045762	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein), clone MGC:9025 IMAGE:3880116, mRNA, complete cds (BC018163.1)	BC018163	Hs.348024	NP_002872
10054	0.028189	similar to hypothetical protein FLJ10883 (LOC115294), mRNA /cds=(98,1171) /gb=NM_052937 /gi=24308385 /ug=Hs.60293 /len=3967	NM_052937	Hs.60293	NP_443169
10080	0.015649	hypothetical protein DKFZp761N0624 (DKFZp761N0624), mRNA /cds=(113,1444) /gb=NM_032295 /gi=14150046 /ug=Hs.21893 /len=2973	NM_032295	Hs.21893	NP_115671

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10100	0.025168	hypothetical protein FLJ22662 (FLJ22662), mRNA /cds=(66,1586) /gb=NM_024829 /gi=13376231 /ug=Hs.178470 /len=1707	NM_024829	Hs.178470	NP_079105
10143	0.043451	phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA /cds=(207,4604) /gb=NM_007366 /gi=19923388 /ug=Hs.171945 /len=5633	NM_007366	Hs.171945	NP_031392
10146	0.037084	EST qz90a06.x1 Soares_pregnant_uterus_NbHPU cDNA clone IMAGE:2041810 3'	AI493872		NP_008878
10151	0.006684	cDNA FLJ36605 fis, clone TRACH2015316, highly similar to VIMENTIN. /cds=(631,1317) /gb=AK093924 /gi=21752883 /ug=Hs.379100 /len=2665	AK093924	Hs.379100	
10205	0.003193	EST (ol74f05.s1 NCI_CGAP_Kid3 cDNA clone IMAGE:1535361 3')	AA919165		
10208	0.004048	cDNA FLJ33503 fis, clone BRAMY2004521. /cds=(367,750) /gb=AK090822 /gi=21749052 /ug=Hs.356719 /len=2339	AK090822	Hs.356719	NP_787089
10228	0.004357	hypothetical protein FLJ10342 (FLJ10342), mRNA /cds=(534,1145) /gb=NM_018064 /gi=14149717 /ug=Hs.101514 /len=1506	NM_018064	Hs.101514	NP_060534
10247	0.002773	vimentin (VIM) gene	M18895		
10277	0.039115	likely ortholog of mouse embryonic epithelial gene 1 (EEG1), mRNA /cds=(319,1794) /gb=NM_017611 /gi=18252046 /ug=Hs.274453 /len=2630	NM_017611	Hs.274453	NP_060081
10315	0.035141	EST (MR0-HT0407-010200-008-g12 HT0407	BE159321		
10323	0.006234	mRNA; cDNA DKFZp434K1115 (from clone DKFZp434K1115); complete cds /cds=(97,2877) /gb=AL136764 /gi=12053044 /ug=Hs.42676 /len=4868	AL136764	Hs.42676	
10351	0.021147	EST (IL2-UM0076-070400-061-F10 UM0076)	AW802800		
10358	0.033283	cDNA, 5' end /clone=IMAGE:4148900 /clone_end=5' /gb=BF342391 /gi=11289392 /ug=Hs.30469 /len=803	BF342391	Hs.30469	NP_055313
10385	0.045762	chondroitin sulfate GalNAcT-2 (GALNACT-2), mRNA /cds=(336,1964) /gb=NM_018590 /gi=24429591 /ug=Hs.180758 /len=3745	NM_018590	Hs.180758	NP_061060
10392	0.012175	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10430	0.017682	EST(ha63a03.x1 NCI_CGAP_Pan1 cDNA clone IMAGE:2878348 3')	AW338626		NP_006826
10432	0.010023	UI-H-BW0-ajd-b-12-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2731343 3', mRNA sequence /clone=IMAGE:2731343 /clone_end=3' /gb=AW297162 /gi=6703808 /ug=Hs.438076 /len=690	AW297162	Hs.438076	
10456	0.045762	mRNA; cDNA DKFZp451D112 (from clone DKFZp451D112); complete cds /cds=(316,4719) /gb=AL831962 /gi=21732493 /ug=Hs.202949 /len=5391	AL831962	Hs.202949	
10503	0.003487	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556	NM_021109	Hs.75968	NP_066932
10536	0.005658	nascent-polypeptide-associated complex alpha polypeptide (NACA), mRNA /cds=(26,673) /gb=NM_005594 /gi=5031930 /ug=Hs.32916 /len=797	NM_005594	Hs.32916	NP_005585
10565	0.048172	clone IMAGE:5284350, mRNA /gb=BC037924 /gi=23138690 /ug=Hs.143061 /len=2659	BC037924	Hs.143061	
10566	0.023762	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
10601	0.004048	EST(cDNA clone IMAGE:3566688 3')	BF110315		NP_002154
10627	0.013819	602584221F1 NIH_MGC_76 cDNA clone IMAGE:4712140 5', mRNA sequence /clone=IMAGE:4712140 /clone_end=5' /gb=BG564543 /gi=13572195 /ug=Hs.105449 /len=981	BG564543	Hs.105449	
10632	0.010701	UI-H-EI1-aze-g-21-0-UI.s1 NCI_CGAP_EI1 cDNA clone IMAGE:5847596 3', mRNA sequence /clone=IMAGE:5847596 /clone_end=3' /gb=BQ003542 /gi=19728442 /ug=Hs.190642 /len=1086	BQ003542	Hs.190642	
10660	0.023762	BX111472 Soares_senescent_fibroblasts_NbHSF cDNA clone IMAGp998B18737, mRNA sequence /clone=IMAGp998B18737_/_IMAGE:325169 /gb=BX111472 /gi=27878522 /ug=Hs.56025 /len=714	BX111472	Hs.56025	
10697	0.021147	EST(PM0-HT0913-100401-013-c08 HT0913 cDNA, MRNA sequence)	BG998053		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10771	0.039257	HUM515D03B Clontech placenta polyA mRNA (#6518) cDNA clone GEN-515D03 5', mRNA sequence /clone=GEN-515D03 /clone_end=5' /gb=D58893 /gi=968527 /ug=Hs.335953 /len=365	D58893	Hs.335953	
10779	0.01471	EST (ADB cDNA clone ADBAKA02 5')	AV704531		
10780	0.037084	hypothetical protein FLJ10300 (FLJ10300), mRNA /cds=(1710,3359) /gb=NM_018051 /gi=21361686 /ug=Hs.42233 /len=3785	NM_018051	Hs.42233	NP_060521
10793	0.041237	im56f03.y1 HR85 islet cDNA clone IMAGE:6039292 5', mRNA sequence /clone=IMAGE:6039292 /clone_end=5' /gb=CA773752 /gi=26011160 /ug=Hs.380642 /len=630	CA773752	Hs.380642	
10794	0.002773	FSHD region gene 1 (FRG1), mRNA /cds=(192,968) /gb=NM_004477 /gi=4758403 /ug=Hs.203772 /len=1042	NM_004477	Hs.203772	NP_004468
10798	0.016639	EST (ta16g05.x1 NCI_CGAP_Lym5 IMAGE:2044280 3')	AI471814		
10843	0.025168	EST (QV0-ST0236-171299-075-c08 ST0236 cDNA)	AW816517		
10852	0.011417	EST yb28f09.s1 Stratagene fetal spleen #937205) H.sapiens cDNA clone IMAGE:72521 3'	T51639		
10853	6.69E-04	EST(zt89c05.r1 Soares testis NHT clone 729512 5')	AA398038		NP_004632
10862	0.003758	mitochondrion, complete genome	NC_001807		
10864	0.016639	EST (ab81d11.s1 Stratagene fetal retina 937202 IMAGE:853365 3')	AA663308		
10888	2.60E-05	UI-H-DH0-aui-j-10-0-UI.s1 NCI_CGAP_DH0 cDNA clone IMAGE:5871081 3', mRNA sequence /clone=IMAGE:5871081 /clone_end=3' /gb=BM994461 /gi=19719362 /ug=Hs.434057 /len=2059	BM994461	Hs.434057	
10897	0.029809	hypothetical protein FLJ25534 (FLJ25534), mRNA /cds=(297,1145) /gb=NM_153234 /gi=23397511 /ug=Hs.23197 /len=2550	NM_153234	Hs.23197	NP_694966
10912	0.028189	cDNA FLJ34675 fis, clone LIVER2001608. /gb=AK091994 /gi=21750487 /ug=Hs.380100 /len=1725	AK091994	Hs.380100	
10950	0.011417	cDNA FLJ38913 fis, clone NT2NE2008017. /gb=AK096232 /gi=21755673 /ug=Hs.50094 /len=2555	AK096232	Hs.50094	NP_835224
10991	0.028189	ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632	NM_000976	Hs.405042	NP_000967

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10996	0.028189	BX118052 Soares breast 2NbHBst cDNA clone IMAGp998C21252, mRNA sequence /clone=IMAGp998C21252;_IMAGE:158156 /gb=BX118052 /gi=27840946 /ug=Hs.32250 /len=612	BX118052	Hs.32250	
11003	0.002372	cDNA FLJ14832 fis, clone OVARC1001169. /gb=AK027738 /gi=14042638 /ug=Hs.235860 /len=2350	AK027738	Hs.235860	
11011	0.007162	EST(cDNA clone IMAGE:2686869 3')	AW197394		
11016	0.033283	mitochondrion, complete genome	NC_001807		
11030	0.048172	ESTs, cDNA, 3' end /clone=IMAGE:2308223 /clone_end=3' /gb=AI671885 /gi=4851616 /ug=Hs.110855 /len=593	AI671885	Hs.110855	
11032	0.017682	nj38c05.s1 NCI_CGAP_AA1 cDNA clone IMAGE:994760 3' similar to gb:M62424 THROMBIN RECEPTOR PRECURSOR mRNA sequence /clone=IMAGE:994760 /clone_end=3' /gb=AA548630 /gi=2318912 /ug=Hs.105848 /len=555	AA548630	Hs.105848	
11033	0.021147	FLJ30661 fis, clone DFNES2000526 /cds=UNKNOWN /gb=AK055223 /gi=16549904 /ug=Hs.265540 /len=2514	AK055223	Hs.265540	NP_057178
11046	0.017682	wc25f11.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2316237 3', mRNA sequence /clone=IMAGE:2316237 /clone_end=3' /gb=AI678258 /gi=4888440 /ug=Hs.174257 /len=585	AI678258	Hs.174257	
11085	0.008208	EST(cDNA clone IMAGE:2126419 3')	AI435109		
11136	0.016639	clone IMAGE:3138608, mRNA /cds=UNKNOWN /gb=BC007266 /gi=13938277 /ug=Hs.334566 /len=1635	BC007266	Hs.334566	
11138	0.045762	nn90a10.s1 NCI_CGAP_Br2 cDNA clone IMAGE:1098426 3', mRNA sequence /clone=IMAGE:1098426 /clone_end=3' /gb=AA614814 /gi=2467010 /ug=Hs.270700 /len=404	AA614814	Hs.270700	
11148	0.019933	ij23g01.x1 Melton Normalized Islet 4 N4-HIS 1 cDNA clone IMAGE:6135721 3', mRNA sequence /clone=IMAGE:6135721 /clone_end=3' /gb=BQ100789 /gi=20133773 /ug=Hs.372964 /len=568	BQ100789	Hs.372964	
11169	0.018775	nad13a08.x1 NCI_CGAP_Lu24 cDNA clone IMAGE:3365271 3', mRNA sequence /clone=IMAGE:3365271 /clone_end=3' /gb=BF439728 /gi=11452245 /ug=Hs.257883 /len=202	BF439728	Hs.257883	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11218	0.007162	chromosome 3q clone CTD-2650N22, WORKING DRAFT SEQUENCE, 5 unordered pieces	AC108668		
11243	0.029809	apoA polymorphism Kringle IV gene, exons 1 and 2	L14005		
11256	0.045762	cDNA FLJ31919 fis, clone NT2RP7004964. /gb=AK056481 /gi=16551895 /ug=Hs.400872 /len=4013	AK056481	Hs.400872	
11266	9.20E-05	B-cell translocation gene 1, anti-proliferative (BTG1), mRNA /cds=(309,824) /gb=NM_001731 /gi=4502472 /ug=Hs.77054 /len=1783	NM_001731	Hs.77054	NP_001722
11275	0.031506	glucose phosphate isomerase (GPI), mRNA /cds=(104,1780) /gb=NM_000175 /gi=18201904 /ug=Hs.406458 /len=2075	NM_000175	Hs.406458	NP_000166
11299	0.039115	ATX1 antioxidant protein 1 (yeast) (ATOX1), mRNA /cds=(114,320) /gb=NM_004045 /gi=4757803 /ug=Hs.279910 /len=502	NM_004045	Hs.279910	NP_004036
11305	0.010023	tousled-like kinase 2 (TLK2), mRNA /cds=(147,2396) /gb=NM_006852 /gi=11140818 /ug=Hs.57553 /len=3327	NM_006852	Hs.57553	NP_006843
11321	0.039115	transient receptor potential cation channel, subfamily C, member 1 (TRPC1), mRNA /cds=(138,2417) /gb=NM_003304 /gi=27545448 /ug=Hs.250687 /len=4085	NM_003304	Hs.250687	NP_003295
11331	0.017682	cell cycle progression 8 protein (CPR8), mRNA /cds=(13,1140) /gb=NM_004748 /gi=4758047 /ug=Hs.82506 /len=1856	NM_004748	Hs.82506	NP_004739
11335	0.023762	COX11 cytochrome c oxidase assembly protein (yeast) (COX11), nuclear gene encoding mitochondrial protein, mRNA /cds=(48,878) /gb=NM_004375 /gi=17921983 /ug=Hs.241515 /len=2717	NM_004375	Hs.241515	NP_004366
11353	0.005412	mRNA; cDNA DKFZp434E2321 (from clone DKFZp434E2321); partial cds /cds=(1,1051) /gb=AL133619 /gi=6599234 /ug=Hs.29383 /len=3447	AL133619	Hs.29383	
11365	6.45E-05	Rho-specific guanine-nucleotide exchange factor 164 kDa (P164RHOGF), mRNA /cds=(16,6207) /gb=NM_014786 /gi=21361457 /ug=Hs.45180 /len=7540	NM_014786	Hs.45180	NP_055601
11402	0.033283	cytochrome c, somatic (CYCS), mRNA /cds=(61,378) /gb=NM_018947 /gi=21361707 /ug=Hs.169248 /len=3990	NM_018947	Hs.169248	NP_061820

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11422	0.048172	CGI-45 protein (CGI-45), mRNA /cds=(194,1321) /gb=NM_015999 /gi=21361518 /ug=Hs.5298 /len=2108	NM_015999	Hs.5298	NP_057083
11446	0.021147	ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986	NM_004152	Hs.281960	NP_004143
11479	0.033283	B lymphocyte activation-related protein BC-2048	AAL26788		
11482	0.013819	clone IMAGE:5271722, mRNA /gb=BC038786 /gi=24270905 /ug=Hs.190456 /len=1535	BC038786	Hs.190456	
11498	0.048653	clone MGC:16614 IMAGE:4111344, mRNA, complete cds /cds=(258,998) /gb=BC009313 /gi=14424569 /ug=Hs.373515 /len=2052	BC009313	Hs.193700	
11503	0.045762	hypothetical protein DKFZp564K0822 (DKFZP564K0822), mRNA /cds=(10,528) /gb=NM_030796 /gi=13540577 /ug=Hs.4750 /len=2789	NM_030796	Hs.4750	NP_110423
11519	0.008208	mRNA; cDNA DKFZp761O0611 (from clone DKFZp761O0611) /gb=AL834155 /gi=21739631 /ug=Hs.22969 /len=4502	AL834155	Hs.22969	
11539	0.041237	mRNA for KIAA1327 protein, partial cds. /cds=(1,5417) /gb=AB037748 /gi=20521883 /ug=Hs.106204 /len=6687	AB037748	Hs.106204	
11608	0.029809	EST(MR0-HT0407-140300-013-h01 HT0407)	BE159552		NP_003751
11615	0.048172	mRNA for KIAA0261 gene, partial cds. /cds=(1,3866) /gb=D87450 /gi=1665788 /ug=Hs.154978 /len=6155	D87450	Hs.154978	
11616	0.030757	EST qz49d11.x1 NCI_CGAP_Kid11 IMAGE:2030229 3'	AI493076		
11634	0.003233	hypothetical protein FLJ12118 (FLJ12118), mRNA /cds=(24,1718) /gb=NM_024537 /gi=13375694 /ug=Hs.381043 /len=1843	NM_024537	Hs.381043	NP_078813
11691	0.023762	cDNA sequence cDNA sequence DKFZp434D0935 (from clone cDNA sequence DKFZp434D0935)	AL117502		NP_149107
11700	0.031506	EST(qh83b09.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:1853561 3')	AI243681		NP_004727
11702	0.023762	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
11720	0.035141	mRNA for KIAA1509 protein, partial cds. /cds=(1,3983) /gb=AB040942 /gi=7959278 /ug=Hs.201500 /len=5283	AB040942	Hs.201500	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11783	0.015649	cDNA FLJ20709 fis, clone KAIA1124, highly similar to D86324 mRNA for CMP-N-acetylneuraminic acid. /gb=AK000716 /gi=7020978 /ug=Hs.24697 /len=3488	AK000716	Hs.24697	
11784	0.004687	sperm associated antigen 9 (SPAG9), transcript variant 1, mRNA /cds=(79,4002) /gb=NM_003971 /gi=27436919 /ug=Hs.129872 /len=4663	NM_003971	Hs.129872	NP_758853
11788	0.019933	Bardet-Biedl syndrome 2 (BBS2), mRNA /cds=(422,2587) /gb=NM_031885 /gi=22208996 /ug=Hs.332633 /len=2978	NM_031885	Hs.332633	NP_114091
11797	0.013819	UI-E-C10-aae-d-12-0-UI.s1 UI-E-C10 cDNA clone UI-E-C10-aae-d-12-0-UI 3', mRNA sequence /clone=UI-E-C10-aae-d-12-0-UI /clone_end=3' /gb=BM663444 /gi=18968780 /ug=Hs.395779 /len=1260	BM663444	Hs.395779	
11811	0.039115	FLJ11481 fis, clone HEMBA1001803 /cds=UNKNOWN /gb=AK021543 /gi=10432744 /ug=Hs.135159 /len=1539	AK021543	Hs.135159	
11816	0.019933	likely ortholog of rat V-1 protein (V-1), mRNA /cds=(229,585) /gb=NM_145808 /gi=21956644 /ug=Hs.21321 /len=3770	NM_145808	Hs.21321	NP_665807
11822	0.006234	protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C), mRNA /cds=(89,1633) /gb=NM_002719 /gi=4506022 /ug=Hs.171734 /len=4064	NM_002719	Hs.171734	NP_848703
11830	0.035141	DKFZp564P2064_s1 564 (synonym: hfbr2) cDNA clone DKFZp564P2064 3', mRNA sequence /clone=DKFZp564P2064 /clone_end=3' /gb=AL037172 /gi=5406623 /ug=Hs.328612 /len=682	AL037172	Hs.328612	
11839	0.015649	proteasome (prosome, macropain) 26S subunit, ATPase, 2 (PSMC2), mRNA /cds=(71,1372) /gb=NM_002803 /gi=24430152 /ug=Hs.61153 /len=1545	NM_002803	Hs.61153	NP_002794
11851	0.041237	mitochondrion, complete genome	NC_001807		
11860	0.009383	FOXJ2 forkhead factor (FHX), mRNA /cds=(490,2214) /gb=NM_018416 /gi=8923841 /ug=Hs.120844 /len=4873	NM_018416	Hs.120844	NP_060886
11865	0.039115	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA /cds=(407,1972) /gb=NM_000944 /gi=19923130 /ug=Hs.272458 /len=4425	NM_000944	Hs.272458	NP_000935

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11875	0.045762	general transcription factor IIIC, polypeptide 3, 102kDa (GTF3C3), mRNA /cds=(94,2754) /gb=NM_012086 /gi=6912397 /ug=Hs.90847 /len=2961	NM_012086	Hs.90847	NP_036218
11876	0.047799	immediate early response 3 (IER3), transcript variant long, mRNA /cds=(30,611) /gb=NM_052815 /gi=16554596 /ug=Hs.76095 /len=1345	NM_052815	Hs.76095	NP_434702
11897	0.037084	hypothetical protein FLJ20701 (FLJ20701), mRNA /cds=(39,938) /gb=NM_017933 /gi=8923631 /ug=Hs.424598 /len=2284	NM_017933	Hs.424598	NP_060403
11921	0.028189	hypothetical protein DKFZp762O076 (DKFZp762O076), mRNA /cds=(77,850) /gb=NM_018710 /gi=24308164 /ug=Hs.21621 /len=2266	NM_018710	Hs.21621	NP_061180
11927	0.005038	CCR4-NOT transcription complex, subunit 8 (CNOT8), mRNA /cds=(245,1123) /gb=NM_004779 /gi=24496777 /ug=Hs.26703 /len=2489	NM_004779	Hs.26703	NP_004770
11938	0.022422	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 S. cerevisiae) (BTAF1), mRNA /cds=(118,5667) /gb=NM_003972 /gi=27477069 /ug=Hs.180930 /len=6345	NM_003972	Hs.180930	NP_003963
11939	0.043451	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747	NM_012479	Hs.25001	NP_036611
11963	0.022422	proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813 /gi=5802981 /ug=Hs.75969 /len=2061	NM_006813	Hs.75969	NP_006804
11979	0.003594	chromosome 20 open reading frame 6 (C20orf6), mRNA /cds=(109,2664) /gb=NM_016649 /gi=22507381 /ug=Hs.88820 /len=3216	NM_016649	Hs.88820	NP_057733
12079	0.023762	EST nj89e12.s1 NCI_CGAP_Pr11 cDNA clone IMAGE:999694	AA552262		
12085	0.033283	retinoic acid induced 14 (RAI14), mRNA /cds=(112,3054) /gb=NM_015577 /gi=13470085 /ug=Hs.15165 /len=4925	NM_015577	Hs.15165	NP_056392
12123	0.031506	UI-H-BI0-aaa-f-10-0-UI.s1 NCI_CGAP_Sub1 cDNA clone IMAGE:2708874 3', mRNA sequence /clone=IMAGE:2708874 /clone_end=3' /gb=AW014102 /gi=5862859 /ug=Hs.304671 /len=654	AW014102	Hs.304671	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12231	0.01471	EST (UI-H-BI3-akf-b-05-0-UI.s1 NCI_CGAP_Sub5 clone IMAGE:2734017 3')	AW449060		NP_061174
12257	0.033283	EST390958 MAGE resequences, MAGP cDNA, mRNA sequence /gb=AW978849 /gi=8170126 /ug=Hs.124977 /len=678	AW978849	Hs.124977	
12259	0.048172	EST (Similar to pleckstrin homology, Sec7 and coiled/coil domains 3, clone MGC:5340 IMAGE:2984886, complete cds /cds=(3,542) /gb=BC008191 /gi=14198262/ug=Hs.7984 /len=3720)	BC008191	Hs.7984	NP_004218
12297	0.026643	hypothetical protein MGC10744 (MGC10744), mRNA /cds=(77,184) /gb=NM_032354 /gi=14150156 /ug=Hs.25092 /len=1212	NM_032354	Hs.25092	NP_115730
12320	0.037084	EST(EST178403 Colon carcinoma (HCC) cell line cDNA 5' end similar to similar to ribosomal protein L30)	AA307521		NP_000980
12346	0.048172	selenoprotein H (SELH), mRNA /cds=(243,611) /gb=NM_170746 /gi=25014108 /ug=Hs.290874 /len=834	NM_170746	Hs.290874	NP_734467
12352	0.021147	UI-H-BI2-ahm-d-05-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2727224 3', mRNA sequence /clone=IMAGE:2727224 /clone_end=3' /gb=AW293452 /gi=6700088 /ug=Hs.16228 /len=634	AW293452	Hs.16228	
12355	0.021147	cDNA FLJ36238 fis, clone THYMU2001422. /gb=AK093557 /gi=21752458 /ug=Hs.345588 /len=2269	AK093557	Hs.345588	
12371	0.041237	ESTs, cDNA, 5' end /clone=BMFBFE06 /clone_end=5' /gb=AV756341 /gi=10914189 /ug=Hs.244273 /len=766	AV756341	Hs.244273	
12375	0.037157	UI-H-DT0-avk-p-22-0-UI.s1 NCI_CGAP_DT0 cDNA clone IMAGE:5880837 3', mRNA sequence /clone=IMAGE:5880837 /clone_end=3' /gb=BM996358 /gi=19721259 /ug=Hs.433458 /len=838	BM996358	Hs.433458	
12395	0.007162	SH3-domain binding protein 4 (SH3BP4), mRNA /cds=(336,3227) /gb=NM_014521 /gi=7657561 /ug=Hs.17667 /len=5145	NM_014521	Hs.17667	NP_055336
12399	0.001721	UI-E-CK1-afh-b-14-0-UI.r1 UI-E-CK1 cDNA clone UI-E-CK1-afh-b-14-0-UI 5', mRNA sequence /clone=UI-E-CK1-afh-b-14-0-UI /clone_end=5' /gb=BM702699 /gi=19015957 /ug=Hs.446508 /len=1088	BM702699	Hs.446508	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12412	0.001133	cDNA / IL3-NT0294-060401-533-D04 NT0294	BI041924		
12430	0.004687	mRNA; cDNA DKFZp686J19116 (from clone DKFZp686J19116) /gb=AL833458 /gi=21734100 /ug=Hs.428760 /len=3297	AL833458	Hs.428760	
12431	0.043451	ESTs, cDNA /gb=AW993259 /gi=8253410 /ug=Hs.113105 /len=678	AW993259	Hs.113105	
12432	0.037084	BX102166 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGp998H154200, mRNA sequence /clone=IMAGp998H154200_/_IMAGE:1655102 /gb=BX102166 /gi=27845155 /ug=Hs.131494 /len=724	BX102166	Hs.131494	
12435	0.045762	clone IMAGE:5263531, mRNA /gb=BC037740 /gi=22902216 /ug=Hs.18016 /len=5036	BC037740	Hs.18016	
12439	0.048653	cDNA FLJ12048 fis, clone HEMBB1001990. /gb=AK022110 /gi=10433433 /ug=Hs.289044 /len=1805	AK022110	Hs.289044	
12465	0.022422	ESTs, cDNA, 5' end /clone=IMAGE:3922401 /clone_end=5' /gb=BE894201 /gi=10356330 /ug=Hs.176376 /len=916	BE894201	Hs.176376	
12484	0.04068	qa50a08.x1 Soares_NhHMPu_S1 cDNA clone IMAGE:1690166 3', mRNA sequence /clone=IMAGE:1690166 /clone_end=3' /gb=AI123569 /gi=3539335 /ug=Hs.117060 /len=773	AI123569	Hs.117060	
12501	0.015649	EST(cDNA clone IMAGE:4693130 5')	BG539987		NP_005397
12513	0.00767	AGENCOURT_8841454 Lupski_sciatic_nerve cDNA clone IMAGE:6199422 5', mRNA sequence /clone=IMAGE:6199422 /clone_end=5' /gb=BQ924341 /gi=22339372 /ug=Hs.442591 /len=930	BQ924341	Hs.442591	
12514	0.041237	DCBCQH10 DCB cDNA, mRNA sequence /gb=BU198777 /gi=22717083 /ug=Hs.50273 /len=867	BU198777	Hs.50273	
12574	1.92E-04	UI-H-ED0-awx-b-15-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5824814 3', mRNA sequence /clone=IMAGE:5824814 /clone_end=3' /gb=BQ020068 /gi=19755345 /ug=Hs.396278 /len=1351	BQ020068	Hs.396278	
12580	0.035141	No significant match	SEQ.ID.No.34		
12609	0.010265	Similar to hypothetical protein FLJ31322, clone IMAGE:5296647, mRNA /gb=BC045189 /gi=28277118 /ug=Hs.350001 /len=2971	BC045189	Hs.350001	NP_787112

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12656	0.035141	hypothetical protein DKFZp564B1162 (DKFZP564B1162), mRNA /cds=(661,2628) /gb=NM_031305 /gi=13775229 /ug=Hs.93589 /len=4593	NM_031305	Hs.93589	NP_112595
12664	0.010023	hypothetical protein FLJ12888 (FLJ12888), mRNA /cds=(333,2210) /gb=NM_024945 /gi=13376426 /ug=Hs.284137 /len=3413	NM_024945	Hs.284137	NP_079221
12695	0.025168	mitochondrion, complete genome	NC_001807		
12720	0.012975	mRNA; cDNA DKFZp667O1616 (from clone DKFZp667O1616) /gb=AL713722 /gi=19584452 /ug=Hs.365655 /len=1773	AL713722	Hs.365655	
12725	2.60E-04	EST(CM3-BN0151-130400-146-f01_1 BN0151)	BE008220		
12734	0.023762	mRNA for FLJ00201 protein. /cds=(1,2119) /gb=AK074129 /gi=18676605 /ug=Hs.353001 /len=4443	AK074129	Hs.353001	
12739	0.022422	xn86b03.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2701325 3', mRNA sequence /clone=IMAGE:2701325 /clone_end=3' /gb=AW195867 /gi=6475097 /ug=Hs.370978 /len=571	AW195867	Hs.370978	
12743	0.041237	EST (RC3-BN0036-090200-011-h11 BN0036 cDNA)	AW994082		
12750	0.019933	mRNA; cDNA DKFZp667H216 (from clone DKFZp667H216) /gb=AL833204 /gi=21733834 /ug=Hs.356145 /len=3782	AL833204	Hs.356145	
12794	0.039115	ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632	NM_000976	Hs.405042	NP_000967
12797	0.026643	EST(xu17f02.x1 NCI_CGAP_Co14 cDNA clone IMAGE:2800443 3')	AW272306		NP_002201
12798	0.015649	UI-H-DF0-bem-a-10-0-UI.s1 NCI_CGAP_DF0 cDNA clone UI-H-DF0-bem-a-10-0-UI 3', mRNA sequence /clone=UI-H-DF0-bem-a-10-0-UI /clone_end=3' /gb=CA425521 /gi=24788247 /ug=Hs.411829 /len=1131	CA425521	Hs.411829	
12835	0.013819	AGENCOURT_8856629 Lupski_sciatic_nerve cDNA clone IMAGE:6200636 5', mRNA sequence /clone=IMAGE:6200636 /clone_end=5' /gb=BQ947179 /gi=22362657 /ug=Hs.356605 /len=1277	BQ947179	Hs.356605	
12843	0.008208	cDNA clone IMAGE:123789 3' similar to contains Alu repetitive element;contains THR repetitive element ; Soares fetal liver spleen 1NFLS	R01434		
12847	0.041237	EST(cDNA clone IMAGE:4472298 5')	BG251774		NP_598001

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12848	0.006762	cDNA: FLJ23165 fis, clone LNG09846. /gb=AK026818 /gi=10439763 /ug=Hs.279898 /len=2117	AK026818	Hs.279898	
12871	0.048172	wg97c03.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2379172 3' similar to contains L1.b1 L1 repetitive element ;, mRNA sequence /clone=IMAGE:2379172 /clone_end=3' /gb=AI762342 /gi=5178009 /ug=Hs.304298 /len=531	AI762342	Hs.304298	
12882	0.026643	DKFZp564A2463 (from clone DKFZp564A2463) /cds=UNKNOWN /gb=AL137573 /gi=6808283 /ug=Hs.43143 /len=1320	AL137573	Hs.43143	
12891	0.045762	cDNA FLJ38472 fis, clone FEBRA2022148. /gb=AK095791 /gi=21755125 /ug=Hs.50150 /len=2454	AK095791	Hs.50150	
12892	0.004048	ESTs, cDNA, 5' end /clone=IMAGE:1554245 /clone_end=5' /gb=AI792925 /gi=5340641 /ug=Hs.137097 /len=585	AI792925	Hs.137097	
12898	0.025168	603395193F1 NIH_MGC_90 cDNA clone IMAGE:5405278 5', mRNA sequence /clone=IMAGE:5405278 /clone_end=5' /gb=BI871283 /gi=16044958 /ug=Hs.443147 /len=845	BI871283	Hs.443147	
12907	0.045762	UI-E-EO0-ahy-j-09-0-UI.r1 UI-E-EO0 cDNA clone UI-E-EO0-ahy-j-09-0-UI 5', mRNA sequence /clone=UI-E-EO0-ahy-j-09-0-UI /clone_end=5' /gb=BM722772 /gi=19043589 /ug=Hs.433569 /len=1166	BM722772	Hs.433569	
12961	0.028189	yp92f09.r1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:194921 5', mRNA sequence /clone=IMAGE:194921 /clone_end=5' /gb=R91059 /gi=958599 /ug=Hs.330761 /len=430	R91059	Hs.330761	
13007	0.023762	EST(cDNA clone GKCAHD03 5')	AV696986		NP_072179
13042	0.033283	EST(cDNA clone IMAGE:4717063 5')	BG569807		
13065	0.003487	control			
13109	0.025168	cDNA FLJ13752 fis, clone PLACE3000352. /gb=AK023814 /gi=10435863 /ug=Hs.144871 /len=3904	AK023814	Hs.144871	
13110	5.57E-04	hypothetical protein P1 p373c6 (P1P373C6), mRNA /cds=(254,1891) /gb=NM_019110 /gi=17738284 /ug=Hs.44720 /len=2316	NM_019110	Hs.44720	NP_061983

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13127	0.035141	brain abundant, membrane attached signal protein 1 (BASP1), mRNA /cds=(53,736) /gb=NM_006317 /gi=5453749 /ug=Hs.79516 /len=1486	NM_006317	Hs.79516	NP_006308
13139	0.035141	chromosome 1 open reading frame 8 (C1orf8), mRNA /cds=(251,1222) /gb=NM_004872 /gi=27545320 /ug=Hs.416495 /len=1709	NM_004872	Hs.416495	NP_004863
13151	0.039115	cell division cycle associated 4 (CDCA4), transcript variant 1, mRNA /cds=(164,889) /gb=NM_017955 /gi=22027508 /ug=Hs.34045 /len=2171	NM_017955	Hs.34045	NP_663747
13160	0.011417	retinoid X receptor, beta (RXRB), mRNA /cds=(180,1781) /gb=NM_021976 /gi=27436942 /ug=Hs.79372 /len=2892	NM_021976	Hs.79372	NP_068811
13161	0.00767	hypothetical protein FLJ10035 (FLJ10035), mRNA /cds=(251,1132) /gb=NM_030803 /gi=24475809 /ug=Hs.16390 /len=2404	NM_030803	Hs.16390	NP_110430
13188	0.001867	hypothetical protein PRO2013 (PRO2013), mRNA /cds=(136,381) /gb=NM_021243 /gi=24308272 /ug=Hs.238205 /len=876	NM_021243	Hs.238205	
13193	0.048172	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA), mRNA /cds=(210,1139) /gb=NM_002715 /gi=4506016 /ug=Hs.91773 /len=2181	NM_002715	Hs.91773	NP_002706
13206	0.005412	spinal cord-derived growth factor-B (SCDGF-B), transcript variant 1, mRNA /cds=(176,1288) /gb=NM_025208 /gi=15451919 /ug=Hs.112885 /len=3808	NM_025208	Hs.112885	NP_149126
13207	0.002024	ARP8 actin-related protein 8 (yeast) (ACTR8), mRNA /cds=(5,1129) /gb=NM_022899 /gi=12597636 /ug=Hs.124219 /len=2797	NM_022899	Hs.124219	NP_075050
13225	0.017682	hypothetical protein MGC4276 similar to CG8198 (MGC4276), mRNA /cds=(70,462) /gb=NM_030940 /gi=24475709 /ug=Hs.177776 /len=1978	NM_030940	Hs.177776	NP_112202
13227	0.033283	cysteine dioxygenase, type I (CDO1), mRNA /cds=(255,857) /gb=NM_001801 /gi=4502754 /ug=Hs.3229 /len=1556	NM_001801	Hs.3229	NP_001792
13302	0.025168	nuclear pore complex protein (NUP107), mRNA /cds=(116,2893) /gb=NM_020401 /gi=9966880 /ug=Hs.236204 /len=3131	NM_020401	Hs.236204	NP_065134

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13304	0.029809	w127d01.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2426113 3', mRNA sequence /clone=IMAGE:2426113 /clone_end=3' /gb=AI866216 /gi=5530323 /ug=Hs.413738 /len=133	AI866216	Hs.413738	
13309	0.01471	nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA /cds=(217,3171) /gb=NM_000901 /gi=4505198 /ug=Hs.1790 /len=5749	NM_000901	Hs.1790	NP_000892
13319	0.004357	cDNA FLJ33540 fis, clone BRAMY2007613. /gb=AK090859 /gi=21749098 /ug=Hs.21213 /len=2030	AK090859	Hs.21213	
13357	0.005811	mRNA; cDNA DKFZp451B1418 (from clone DKFZp451B1418) /gb=AL832622 /gi=21733197 /ug=Hs.446489 /len=5612	AL832622	Hs.446489	
13425	0.025168	EST(wk79e07.x1 NCI_CGAP_Pan1 clone IMAGE:2421636 3')	AI813780		
13453	0.035141	mesoderm induction early response 1 (MIR1), mRNA /cds=(234,1844) /gb=NM_020948 /gi=24308260 /ug=Hs.222746 /len=4972	NM_020948	Hs.222746	NP_065999
13457	0.045762	translin (TSN), mRNA /cds=(236,922) /gb=NM_004622 /gi=20302160 /ug=Hs.75066 /len=3408	NM_004622	Hs.75066	NP_004613
13459	0.039115	N-ethylmaleimide-sensitive factor (NSF), mRNA /cds=(61,2295) /gb=NM_006178 /gi=11079227 /ug=Hs.108802 /len=3960	NM_006178	Hs.108802	NP_006169
13467	0.010701	EST(z104d06.r1 NCI_CGAP_GCB1 clone IMAGE:712139 5')	AA280235		NP_005728
13469	0.029809	clone IMAGE:5299642, mRNA /gb=BC041913 /gi=27469540 /ug=Hs.17132 /len=2227	BC041913	Hs.17132	
13501	0.007162	likely ortholog of mouse WD-40-repeat-containing protein with a SOCS box 2 (WSB2), mRNA /cds=(66,1280) /gb=NM_018639 /gi=20149658 /ug=Hs.136644 /len=2610	NM_018639	Hs.136644	NP_061109
13513	0.015649	EST(PM3-SN0020-270300-001-h08 SN0020)	AW865025		NP_115668
13520	0.031506	EST(tz32c11.x1 NCI_CGAP_Ut2 clone IMAGE:2290292 3')	AI631079		NP_079436
13522	0.021147	mRNA; cDNA DKFZp451O1818 (from clone DKFZp451O1818) /gb=AL832650 /gi=21733226 /ug=Hs.12396 /len=4870	AL832650	Hs.12396	
13530	7.32E-04	synaptic nuclei expressed gene 1 (SYNE-1), transcript variant beta, mRNA /cds=(121,10086) /gb=NM_015293 /gi=19526752 /ug=Hs.192102 /len=10742	NM_015293	Hs.192102	NP_598411

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13562	0.041237	AGENCOURT_6653840 NIH_MGC_116 cDNA clone IMAGE:5761286 5', mRNA sequence /clone=IMAGE:5761286 /clone_end=5' /gb=BM924828 /gi=19375207 /ug=Hs.181174 /len=1422	BM924828	Hs.181174	
13599	0.00767	mRNA; cDNA DKFZp313E1012 (from clone DKFZp313E1012) /gb=AL832661 /gi=21733237 /ug=Hs.94694 /len=3233	AL832661	Hs.94694	
13601	0.001234	similar to rat myomegalin (LOC64182), mRNA /cds=(336,1268) /gb=NM_022359 /gi=21314705 /ug=Hs.333512 /len=1717	NM_022359	Hs.333512	NP_071754
13602	0.003758	UI-1-BC1p-asi-a-02-0-UI.s1 NCI_CGAP_PI3 cDNA clone UI-1-BC1p-asi-a-02-0-UI 3', mRNA sequence /clone=UI-1-BC1p-asi-a-02-0-UI /clone_end=3' /gb=BQ011545 /gi=19736446 /ug=Hs.361171 /len=1143	BQ011545	Hs.361171	
13615	0.018779	mRNA full length insert cDNA clone EUROIMAGE 1476475 /gb=AJ420560 /gi=17066424 /ug=Hs.93231 /len=1346	AJ420560	Hs.93231	
13619	0.014281	FLJ30633 fis, clone CTONG2002418, weakly similar to Homo sapiens scaffold attachment factor B (SAF-B) mRNA (AK055195.1)	AK055195	Hs.331328	NP_079031
13642	0.031506	calpastatin (CAST), transcript variant 2, mRNA /cds=(155,2215) /gb=NM_173060 /gi=27765084 /ug=Hs.359682 /len=4296	NM_173060	Hs.359682	NP_775085
13665	0.003758	ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA /cds=(22,459) /gb=NM_003350 /gi=12025664 /ug=Hs.79300 /len=1535	NM_003350	Hs.79300	NP_003341
13670	0.048172	hypothetical protein FLJ11506 (FLJ11506), mRNA /cds=(16,963) /gb=NM_024666 /gi=20070334 /ug=Hs.77703 /len=2774	NM_024666	Hs.77703	NP_078942
13729	0.023762	EH-domain containing 1 (EHD1), mRNA /cds=(247,1851) /gb=NM_006795 /gi=5803008 /ug=Hs.155119 /len=3508	NM_006795	Hs.155119	NP_006786
13731	0.022422	diacylglycerol O-acyltransferase homolog 2 (mouse) (DGAT2), mRNA /cds=(777,1670) /gb=NM_032564 /gi=14211870 /ug=Hs.334305 /len=2713	NM_032564	Hs.334305	NP_115953
13768	0.021586	likely ortholog of mouse hypoxia induced gene 1 (HIG1), mRNA /cds=(93,374) /gb=NM_014056 /gi=7661619 /ug=Hs.7917 /len=1362	NM_014056	Hs.7917	NP_054775
13786	0.011417	mitochondrion, complete genome	NC_001807		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13795	0.045762	hypothetical protein FLJ21302 (FLJ21302), mRNA /cds=(91,1203) /gb=NM_022901 /gi=12597640 /ug=Hs.128071 /len=3160	NM_022901	Hs.128071	NP_075052
13797	0.037084	603041572T1 NIH_MGC_116 cDNA clone IMAGE:5163112 3', mRNA sequence /clone=IMAGE:5163112 /clone_end=3' /gb=BI517954 /gi=15342746 /ug=Hs.398211 /len=964	BI517954	Hs.398211	
13835	0.013819	mRNA for KIAA1078 protein, partial cds. /cds=(1,4098) /gb=AB029001 /gi=20521755 /ug=Hs.23585 /len=6740	AB029001	Hs.23585	
13945	0.018779	EST(tx88e11.x1 NCI_CGAP_Ut4 clone IMAGE:2276684 3' contains Alu repeat)	AI690725		
13961	0.021147	Novel	SEQ.ID.No.90		
13986	0.019933	phosphodiesterase 6D, cGMP-specific, rod, delta (PDE6D), mRNA /cds=(151,603) /gb=NM_002601 /gi=4505670 /ug=Hs.48291 /len=1131	NM_002601	Hs.48291	NP_002592
14059	0.045762	EST (cDNA clone IMAGE:2490676 3')	AI972954		NP_000996
14076	0.023762	hypothetical protein FLJ22611 (FLJ22611), mRNA /cds=(295,1923) /gb=NM_032226 /gi=24308321 /ug=Hs.27774 /len=2821	NM_032226	Hs.27774	NP_115602
14111	0.039115	hypothetical protein MGC3121 (MGC3121), mRNA /cds=(179,1936) /gb=NM_024031 /gi=13128979 /ug=Hs.293629 /len=2063	NM_024031	Hs.293629	NP_076936
14122	0.033283	602152950F1 NIH_MGC_81 cDNA clone IMAGE:4293853 5', mRNA sequence /clone=IMAGE:4293853 /clone_end=5' /gb=BF673050 /gi=11946945 /ug=Hs.208558 /len=830	BF673050	Hs.208558	
14129	0.035141	zu07g05.s1 Soares_testis_NHT cDNA clone IMAGE:731192 3' similar to P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;, mRNA sequence /clone=IMAGE:731192 /clone_end=3' /gb=AA417352 /gi=2077434 /ug=Hs.445851 /len=519	AA417352	Hs.445851	
14132	0.00767	EST (ie64h03.x1 Homo sapiens cDNA, 3' end/clone_end=3' /gb=BI963813 /gi=16338218 /ug=Hs.349015/len=555)	BI963813	Hs.349015	NP_116159
14163	0.016639	EST(AV657608 GLC cDNA clone GLCFDF10 3')	AV657608		
14219	0.041237	cDNA FLJ37978 fis, clone CTONG2010348. /gb=AK095297 /gi=21754529 /ug=Hs.381207 /len=3284	AK095297	Hs.381207	
14249	0.043451	mitochondrion, complete genome	NC_001807		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14266	0.028189	EST, cDNA /clone=IMAGE:1266535 /gb=AA729300 /gi=2750659 /ug=Hs.325555 /len=173	AA729300	Hs.325555	
14268	0.037084	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D), transcript variant 1, mRNA /cds=(505,1941) /gb=NM_172127 /gi=26667185 /ug=Hs.111460 /len=4098	NM_172127	Hs.111460	NP_742126
14294	0.035141	decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=NM_001920 /gi=19743844 /ug=Hs.433989 /len=1751	NM_001920	Hs.433989	NP_598014
14295	0.011417	cDNA: FLJ22765 fis, clone KAIA1180. /gb=AK026418 /gi=10439279 /ug=Hs.163986 /len=1994	AK026418	Hs.163986	
14375	8.74E-04	ESTs, cDNA, 3' end /clone=IMAGE:2402646 /clone_end=3' /gb=AI768858 /gi=5235367 /ug=Hs.157149 /len=562	AI768858	Hs.157149	NP_066012
14386	0.004357	UI-E-EJ0-aik-i-20-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-aik-i-20-0-UI 5', mRNA sequence /clone=UI-E-EJ0-aik-i-20-0-UI /clone_end=5' /gb=BM727413 /gi=19048746 /ug=Hs.112619 /len=1667	BM727413	Hs.112619	
14387	0.016639	likely ortholog of rat V-1 protein (V-1), mRNA /cds=(229,585) /gb=NM_145808 /gi=21956644 /ug=Hs.21321 /len=3770	NM_145808	Hs.21321	NP_665807
14417	0.019933	proteasome (prosome, macropain) subunit, alpha type, 4 (PSMA4), mRNA /cds=(137,922) /gb=NM_002789 /gi=23110940 /ug=Hs.251531 /len=1189	NM_002789	Hs.251531	NP_002780
14453	0.023762	NO significant match, ORF+1(16~273)	SEQ.ID.No.41		
14455	0.004357	No significant match, ORF+3(135~404)	SEQ.ID.No.50		
14504	0.021586	No significant match (ORF:none)	SEQ.ID.No.22		
14521	0.036435	HSC15D092 normalized infant brain cDNA cDNA clone c-15d09 3', mRNA sequence /clone=c-15d09 /clone_end=3' /gb=Z39248 /gi=562440 /ug=Hs.27328 /len=352	Z39248	Hs.27328	
14524	0.001721	EST (wa75f06.x1 Soares NFL T GBC S1	AI685268		
14546	4.21E-04	EST (601819273F1 NIH_MGC_58 cDNA clone IMAGE:4051098 5')	BF130672		NP_003655
14549	0.036435	UI-H-BI3-alq-c-04-0-UI.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:3068166 3', mRNA sequence /clone=IMAGE:3068166 /clone_end=3' /gb=BF512182 /gi=11597361 /ug=Hs.196953 /len=864	BF512182	Hs.196953	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14560	0.017682	TRAM-like protein (KIAA0057), mRNA /cds=(76,1188) /gb=NM_012288 /gi=6912449 /ug=Hs.153954 /len=6974	NM_012288	Hs.153954	NP_036420
14614	0.019094	EST(yq95a02.r1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:203498 5' similar to contains Alu repetitive element)	H56096		
14637	0.01471	hypothetical protein PRO1331 (PRO1331), mRNA /cds=(423,617) /gb=NM_030778 /gi=13562115 /ug=Hs.301824 /len=1634	NM_030778	Hs.301824	NP_110405
14704	0.043451	qz33c01.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2028672 3', mRNA sequence /clone=IMAGE:2028672 /clone_end=3' /gb=AI262059 /gi=3870262 /ug=Hs.386784 /len=229	AI262059	Hs.386784	
14833	0.013819	EST380251 MAGE resequences, MAGJ cDNA, mRNA sequence /gb=AW968281 /gi=8158016 /ug=Hs.319460 /len=689	AW968281	Hs.319460	
14837	0.026643	EST(RC4-CT0322-261299-011-h03 CT0322 Homo sapiens cDNA, mRNA sequence)	AW857814		
14842	0.008208	mitochondrion, complete genome	NC_001807		
14864	0.018779	cDNA FLJ31594 fis, clone NT2RI2002507	AK056156		NP_006818
14934	0.007918	No significant match (ORF:+1:1~102[102])	SEQ.ID.No.59		
14942	0.005811	EST, cDNA /gb=AW360966 /gi=6865616 /ug=Hs.6653 /len=661	AW360966	Hs.6653	NP_055942
14948	0.048172	EST(Fetal Cochlea Homo sapiens cDNA clone IMAGE:2537435 5')	BI497119		NP_006826